

EAST Search History

Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
L1	306	spondin	US-PGPUB; USPAT; EPO; JPO; DERWENT	ADJ	ON	2006/06/14 10:57
L2	249793	antibody or antibodies or immunoglobulin or immunoglobulins	US-PGPUB; USPAT; EPO; JPO; DERWENT	ADJ	ON	2006/06/14 10:57
L3	37	L1 same L2	US-PGPUB; USPAT; EPO; JPO; DERWENT	ADJ	ON	2006/06/14 10:58
L4	149	mindin	US-PGPUB; USPAT; EPO; JPO; DERWENT	ADJ	ON	2006/06/14 10:57
L5	1	L4 same L2	US-PGPUB; USPAT; EPO; JPO; DERWENT	ADJ	ON	2006/06/14 10:58
L6	249793	antibody or antibodies or immunoglobulin or immunoglobulins	US-PGPUB; USPAT; EPO; JPO; DERWENT	ADJ	ON	2006/06/14 10:57
L7	1633	RG1 or (RG-1) or (rg adj "1")	US-PGPUB; USPAT; EPO; JPO; DERWENT	ADJ	ON	2006/06/14 10:57
L8	28	L7 SAME L6	US-PGPUB; USPAT; EPO; JPO; DERWENT	ADJ	ON	2006/06/14 10:57

SCORE Search Results Details for Application 10616279 and Search Result us-10-616-279-2_copy_188_210.rag.

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OM protein - protein search, using sw model

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Run on:      May 25, 2006, 11:55:15 ; Search time 18.8418 Seconds
              (without alignments)
              558.119 Million cell updates/sec
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Title:          US-10-616-279-2_COPY_188_210
Perfect score: 121
Sequence:      1 DAGTDSGFTFSSPNFATIPODTV 23
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
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10: geneseqp2006s:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	121	100.0	23	9	ADW76954	Adw76954 Human RG1
2	121	100.0	249	3	AAB34753	Aab34753 Human sec
3	121	100.0	298	8	ADT50840	Adt50840 Cancer re
4	121	100.0	299	3	AAY73490	Aay73490 Human sec
5	121	100.0	330	4	AAE12304	Aae12304 Human NPG
6	121	100.0	330	9	ADW76932	Adw76932 Rat RG1 p
7	121	100.0	331	2	AAW23663	Aaw23663 Human neu
8	121	100.0	331	2	AAW70589	Aaw70589 Adhesion-
9	121	100.0	331	2	AAW83328	Aaw83328 Human min
10	121	100.0	331	2	AAY41721	Aay41721 Human PRO
11	121	100.0	331	2	AAW92460	Aaw92460 Human NAF
12	121	100.0	331	3	AAB33465	Aab33465 Human PRO
13	121	100.0	331	3	AAY79561	Aay79561 Cancer sp
14	121	100.0	331	3	AAB44277	Aab44277 Human PRO
15	121	100.0	331	3	AAY95349	Aay95349 Human PRO
16	121	100.0	331	4	AAM93266	Aam93266 Human pol
17	121	100.0	331	4	AAM93324	Aam93324 Human pol
18	121	100.0	331	4	AAM38872	Aam38872 Human pol
19	121	100.0	331	4	AAB82472	Aab82472 Human ext
20	121	100.0	331	5	ABG61806	Abg61806 Prostate
21	121	100.0	331	5	AAU79944	Aau79944 Human Spo
22	121	100.0	331	5	ABB77393	Abb77393 Human spo
23	121	100.0	331	5	AAE20463	Aae20463 Human tum
24	121	100.0	331	6	ABO25223	Abo25223 Novel hum
25	121	100.0	331	6	ABU72229	Abu72229 Novel hum
26	121	100.0	331	6	ABU84909	Abu84909 Human sec
27	121	100.0	331	6	ABU61107	Abu61107 Human PRO
28	121	100.0	331	6	ABU80376	Abu80376 Human sec
29	121	100.0	331	6	ABG75949	Abg75949 Human ant
30	121	100.0	331	6	ADA24775	Ada24775 Novel hum
31	121	100.0	331	6	ABO19678	Abo19678 Novel hum
32	121	100.0	331	6	ADA12436	Ada12436 Human sec
33	121	100.0	331	6	ABO19569	Abo19569 Novel hum
34	121	100.0	331	7	ADB73742	Adb73742 Human PRO
35	121	100.0	331	7	ADB76458	Adb76458 Human PRO
36	121	100.0	331	7	ADB75561	Adb75561 Prostate
37	121	100.0	331	7	ADC43884	Adc43884 Human sec
38	121	100.0	331	7	ADC61644	Adc61644 Human sec
39	121	100.0	331	7	ADC63608	Adc63608 Human sec
40	121	100.0	331	7	ADC66708	Adc66708 Human sec
41	121	100.0	331	7	ADC68832	Adc68832 Human sec
42	121	100.0	331	7	ADC62892	Adc62892 Human sec
43	121	100.0	331	7	ADC67957	Adc67957 Human sec
44	121	100.0	331	7	ADC41277	Adc41277 Human sec
45	121	100.0	331	7	ADC67332	Adc67332 Human sec

ALIGNMENTS

RESULT 1

ADW76954

ID ADW76954 standard; peptide; 23 AA.

XX

AC ADW76954;

XX

DT 07-APR-2005 (first entry)

SCORE Search Results Details for Application 10616279 and Search Result us-10-616-279- 2_copy_188_210.ra1.

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OM protein - protein search, using sw model

Run on: May 25, 2006, 12:07:05 ; Search time 4.80791 Seconds
(without alignments)
418.728 Million cell updates/sec

Title: US-10-616-279-2_COPY_188_210
Perfect score: 121
Sequence: 1 DAGTDSGFTFSSPNFATIPQDTV 23

Scoring table: BLOSUM62
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Total number of hits satisfying chosen parameters: 650591

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	121	100.0	299	2	US-09-311-021-202	Sequence 202, App
2	121	100.0	330	2	US-09-371-696-2	Sequence 2, Appli
3	121	100.0	330	2	US-09-732-357B-13	Sequence 13, Appl
4	121	100.0	331	1	US-08-799-173A-2	Sequence 2, Appli
5	121	100.0	331	2	US-09-732-357B-2	Sequence 2, Appli
6	121	100.0	331	2	US-09-170-042A-2	Sequence 2, Appli
7	121	100.0	331	2	US-09-949-002-397	Sequence 397, App
8	121	100.0	331	2	US-09-999-833A-236	Sequence 236, App
9	121	100.0	331	2	US-09-807-200-2	Sequence 2, Appli
10	121	100.0	331	2	US-10-020-445A-236	Sequence 236, App
11	121	100.0	331	2	US-09-978-189-236	Sequence 236, App
12	121	100.0	331	2	US-10-017-085A-236	Sequence 236, App
13	121	100.0	331	3	US-10-145-129A-236	Sequence 236, App
14	121	100.0	331	3	US-10-013-929A-236	Sequence 236, App
15	121	100.0	331	3	US-10-013-917A-236	Sequence 236, App
16	121	100.0	422	2	US-09-949-002-504	Sequence 504, App
17	116	95.9	23	2	US-09-732-357B-11	Sequence 11, Appl
18	86	71.1	568	1	US-07-862-021B-14	Sequence 14, Appl
19	86	71.1	568	5	PCT-US93-03164-14	Sequence 14, Appl
20	82	67.8	392	1	US-08-799-173A-7	Sequence 7, Appli
21	82	67.8	392	2	US-09-170-042A-7	Sequence 7, Appli
22	82	67.8	787	2	US-09-825-294-207	Sequence 207, App
23	82	67.8	787	2	US-09-970-966-207	Sequence 207, App
24	82	67.8	807	1	US-07-862-021B-10	Sequence 10, Appl
25	82	67.8	807	1	US-08-313-288B-10	Sequence 10, Appl
26	82	67.8	807	2	US-09-132-769-1	Sequence 1, Appli
27	82	67.8	807	2	US-09-132-769-3	Sequence 3, Appli
28	82	67.8	807	2	US-09-132-769-5	Sequence 5, Appli
29	82	67.8	807	2	US-09-640-173-186	Sequence 186, App
30	82	67.8	807	2	US-09-713-550-186	Sequence 186, App
31	82	67.8	807	2	US-09-825-294-186	Sequence 186, App
32	82	67.8	807	2	US-09-970-966-186	Sequence 186, App
33	82	67.8	807	5	PCT-US93-03164-10	Sequence 10, Appl
34	81	66.9	802	1	US-07-862-021B-12	Sequence 12, Appl
35	81	66.9	802	1	US-08-313-288B-12	Sequence 12, Appl
36	81	66.9	802	5	PCT-US93-03164-12	Sequence 12, Appl
37	61	50.4	23	2	US-09-132-769-19	Sequence 19, Appl
38	55	45.5	677	2	US-09-270-767-58094	Sequence 58094, A
39	55	45.5	847	2	US-09-270-767-42783	Sequence 42783, A
40	54	44.6	819	2	US-09-270-767-42963	Sequence 42963, A
41	48.5	40.1	838	3	US-10-420-191-2	Sequence 2, Appli
42	47	38.8	424	2	US-09-328-352-4377	Sequence 4377, Ap
43	46	38.0	863	2	US-09-619-353-14	Sequence 14, Appl
44	46	38.0	1198	2	US-09-199-637A-405	Sequence 405, App
45	45.5	37.6	489	2	US-09-771-161A-176	Sequence 176, App

ALIGNMENTS

RESULT 1

US-09-311-021-202

; Sequence 202, Application US/09311021

; Patent No. 6706869

; GENERAL INFORMATION:

; APPLICANT: Wong, Gordon G.

; APPLICANT: Clark, Hilary

; APPLICANT: Fechtel, Kim

; APPLICANT: Agostino, Michael J.

; APPLICANT: Genetics Institute, Inc.

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OM protein - protein search, using sw model

Run on: May 25, 2006, 12:23:39 ; Search time 16.048 Seconds
(without alignments)
663.879 Million cell updates/sec

Title: US-10-616-279-2_COPY_188_210
Perfect score: 121
Sequence: 1 DAGTDSGFTFSSPNFATIPQDTV 23

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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No.	Score	Match	Length	DB	ID	Description	

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2	121	100.0	330	3	US-09-970-944-41	Sequence 41, Appl
3	121	100.0	330	4	US-10-616-279-13	Sequence 13, Appl
4	121	100.0	330	4	US-10-624-884-13	Sequence 13, Appl
5	121	100.0	330	5	US-10-895-183-13	Sequence 13, Appl
6	121	100.0	331	3	US-09-732-357A-2	Sequence 2, Appli
7	121	100.0	331	3	US-09-978-295A-236	Sequence 236, App
8	121	100.0	331	3	US-09-938-418-8	Sequence 8, Appli
9	121	100.0	331	3	US-09-978-697-236	Sequence 236, App
10	121	100.0	331	3	US-09-978-192A-236	Sequence 236, App
11	121	100.0	331	3	US-09-999-832A-236	Sequence 236, App
12	121	100.0	331	3	US-09-978-189-236	Sequence 236, App
13	121	100.0	331	3	US-09-978-608A-236	Sequence 236, App
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15	121	100.0	331	3	US-09-978-191A-236	Sequence 236, App
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17	121	100.0	331	3	US-09-978-564A-236	Sequence 236, App
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37	121	100.0	331	3	US-09-978-665A-236	Sequence 236, App
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45	121	100.0	331	4	US-10-017-081A-236	Sequence 236, App

ALIGNMENTS

RESULT 1

US-09-903-383-2

; Sequence 2, Application US/09903383

; Patent No. US20020137135A1

; GENERAL INFORMATION:

; APPLICANT: Sytkowski, Arthur J.

; APPLICANT: Yang, Meiheng

; TITLE OF INVENTION: NOVEL NPG-1 GENE THAT IS DIFFERENTIALLY EXPRESSED IN PROSTATE

; TITLE OF INVENTION: TUMORS

; FILE REFERENCE: 01948/053002

; CURRENT APPLICATION NUMBER: US/09/903,383

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OM protein - protein search, using sw model

Run on: May 25, 2006, 12:23:59 ; Search time 1.03955 Seconds
(without alignments)
246.414 Million cell updates/sec

Title: US-10-616-279-2_COPY_188_210
Perfect score: 121
Sequence: 1 DAGTDSGFTFSSPNFATIPQDTV 23

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 56051 seqs, 11137335 residues

Total number of hits satisfying chosen parameters: 56051

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
- 7: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result %
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3	44	36.4	268	6	US-10-953-349-18733	Sequence 18733, A
4	44	36.4	315	6	US-10-953-349-20835	Sequence 20835, A
5	44	36.4	334	6	US-10-953-349-20834	Sequence 20834, A
6	44	36.4	344	6	US-10-953-349-20833	Sequence 20833, A
7	44	36.4	448	7	US-11-293-697-3667	Sequence 3667, Ap
8	42	34.7	1338	6	US-10-505-928-634	Sequence 634, App
9	42	34.7	1338	6	US-10-505-928-857	Sequence 857, App
10	41	33.9	381	6	US-10-953-349-21878	Sequence 21878, A
11	40	33.1	208	6	US-10-953-349-16383	Sequence 16383, A
12	40	33.1	280	6	US-10-953-349-16382	Sequence 16382, A
13	40	33.1	342	6	US-10-953-349-16381	Sequence 16381, A
14	40	33.1	408	6	US-10-953-349-32202	Sequence 32202, A
15	40	33.1	425	6	US-10-953-349-32201	Sequence 32201, A
16	40	33.1	462	6	US-10-953-349-32200	Sequence 32200, A
17	40	33.1	881	7	US-11-121-154-170	Sequence 170, App
18	39.5	32.6	117	6	US-10-968-757-3	Sequence 3, Appli
19	39.5	32.6	117	6	US-10-968-757-11	Sequence 11, Appl
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21	39	32.2	286	6	US-10-953-349-6607	Sequence 6607, Ap
22	39	32.2	367	7	US-11-253-300-29	Sequence 29, Appl
23	39	32.2	413	6	US-10-953-349-846	Sequence 846, App
24	39	32.2	431	6	US-10-953-349-845	Sequence 845, App
25	38.5	31.8	101	6	US-10-953-349-27180	Sequence 27180, A
26	38.5	31.8	167	6	US-10-953-349-27179	Sequence 27179, A
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32	38	31.4	690	6	US-10-953-349-3548	Sequence 3548, Ap
33	38	31.4	902	6	US-10-953-349-3547	Sequence 3547, Ap
34	38	31.4	1189	7	US-11-311-778-20	Sequence 20, Appl
35	37.5	31.0	290	6	US-10-953-349-3888	Sequence 3888, Ap
36	37.5	31.0	307	6	US-10-953-349-10430	Sequence 10430, A
37	37.5	31.0	351	6	US-10-953-349-10429	Sequence 10429, A
38	37.5	31.0	388	6	US-10-953-349-10428	Sequence 10428, A
39	37.5	31.0	412	6	US-10-953-349-22821	Sequence 22821, A
40	37.5	31.0	442	6	US-10-953-349-22820	Sequence 22820, A
41	37.5	31.0	463	6	US-10-953-349-3887	Sequence 3887, Ap
42	37.5	31.0	469	6	US-10-953-349-3886	Sequence 3886, Ap
43	37	30.6	119	7	US-11-300-563-11	Sequence 11, Appl
44	37	30.6	217	6	US-10-953-349-5801	Sequence 5801, Ap
45	37	30.6	219	6	US-10-953-349-5800	Sequence 5800, Ap

ALIGNMENTS

RESULT 1

US-10-953-349-18735

; Sequence 18735, Application US/10953349

; Publication No. US20060107345A1

; GENERAL INFORMATION:

; APPLICANT: ALEXANDROV, Nickolai et al.

; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDE

; TITLE OF INVENTION: ENCODED THERBY

; FILE REFERENCE: 2750-1579PUS2

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A;Cross-references: UNIPROT:O53444; UNIPARC:UPI00000D5EAA; GB:AL021897; GB:AL123456; AB0221 probable sugar-binding periplasmic protein YPO1813 [imported] - Yersinia pestis (strain CC N.; Holroyd, S.; Jagels, K.; Leather, S.; Karlyshev, A.V.; Moule, S.; Oyston, P.C.F.; Quail, M.; Ruth PID:g15979836; GSPDB:GN00175 C;Genetics: A;Gene: YPO1813 Query Match 38.0%; Score 46; I T10666 R;Bevan, M.; Lennard, N.; Quail, M.; Harris, B.; Rajandream, M.A.; Barrell, B.G.; Bancroft, A;Introns: 47/3; 87/1; 123/3; 203/3; 230/2; 255/3; 284/3; 305/1; 335/3; 347/3; 370/3; 393/3; thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 23-Apr-1999 #sequence_revis source: cultivar Columbia; BAC clone F8D20 C;Genetics: A;Map position: 4 A;Introns: 13/3; 58/2; cytochrome c2, iso-2 - Rhodospirillum molischianum C;Species: Rhodospirillum molischianum C;Da protein A;Residues: 1-97 A;Cross-references: UNIPROT:P00088; UNIPARC:UPI0000128854 C;Supr Conservative 1; Mismatches 3; Indels 0; Gaps 0; Qy 2 AGTDSGFTFSSPN 14 ||| ||| || |: Db 35 AGT ferredoxin from the nonheterocystous, nitrogen-fixing cyanobacterium Plectonema boryanum PCC 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0; Qy 5 DSGFTFSSPN 14 |||| ||:|| Db 88 DSGFKI

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OM protein - protein search, using sw model

Run on: May 25, 2006, 12:00:39 ; Search time 3.11864 Seconds
(without alignments)
709.599 Million cell updates/sec

Title: US-10-616-279-2_COPY_188_210
Perfect score: 121
Sequence: 1 DAGTDSGFTFSSPNFATIPQDTV 23

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0.
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	86	71.1	803	2	A47723	F-spondin precursor
2	82	67.8	807	2	A38152	F-spondin - rat
3	67	55.4	805	2	T34212	hypothetical prote
4	50	41.3	678	2	G65104	hypothetical 72.8
5	50	41.3	678	2	D91132	probable glycosyla
6	50	41.3	678	2	G85977	probable glycosyla
7	48	39.7	118	2	S04873	hypothetical prote
8	47	38.8	135	2	T09238	hypothetical prote
9	47	38.8	237	2	E84211	hypothetical prote
10	46.5	38.4	291	2	F70896	hypothetical prote
11	46	38.0	331	2	AB0221	probable sugar-bin
12	46	38.0	670	2	T10666	hypothetical prote
13	46	38.0	917	2	T04661	hypothetical prote
14	45	37.2	97	1	CCQFM2	cytochrome c2, iso
15	45	37.2	121	2	B49890	fdxH 5'-region hyp
16	45	37.2	291	2	T49260	hypothetical prote
17	45	37.2	312	2	T08282	regulatory protein
18	45	37.2	412	2	C84518	hypothetical prote
19	45	37.2	426	2	C97797	tetrahydrofolylpol
20	45	37.2	901	2	T03726	capsid polyprotein
21	45	37.2	3224	1	S58884	Ran-binding protei
22	44	36.4	103	2	A55223	hypothetical prote
23	44	36.4	117	1	MHDGMO	Ig heavy chain V r
24	44	36.4	433	2	G71657	folylpolyglutamate
25	44	36.4	492	2	A97429	flgK protein prote
26	44	36.4	492	2	AB2647	hook associated pr
27	44	36.4	702	2	T13058	NADH2 dehydrogenas
28	44	36.4	1034	2	T30331	P-glycoprotein - T
29	44	36.4	1265	2	S57968	Ran-binding protei
30	43.5	36.0	1147	2	S64930	serine/threonine-s
31	43	35.5	117	2	H71180	hypothetical prote
32	43	35.5	221	2	AH2510	hypothetical prote
33	43	35.5	372	2	T42535	leucine-tRNA ligas
34	43	35.5	379	2	AI2267	hypothetical prote
35	43	35.5	394	2	G84206	hypothetical prote
36	43	35.5	449	2	G64597	UDP-N-acetylmurama
37	43	35.5	472	2	B56954	yes-associated pro
38	43	35.5	513	2	T38044	hypothetical prote
39	43	35.5	600	2	T38798	hypothetical prote
40	43	35.5	990	2	A86215	protein T6D22.8 [i
41	43	35.5	1038	2	AG2187	hypothetical prote
42	43	35.5	1111	2	T38407	leucyl-trna synthe
43	43	35.5	1819	2	D97033	uncharacterized pr
44	43	35.5	2090	2	S26058	probable transform
45	42.5	35.1	213	2	A84250	NADH oxidase [impo

ALIGNMENTS

RESULT 1

A47723

F-spondin precursor - African clawed frog

C;Species: Xenopus laevis (African clawed frog)

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OM protein - protein search, using sw model

Run on: May 25, 2006, 11:55:28 ; Search time 24.9492 Seconds
(without alignments)
852.749 Million cell updates/sec

Title: US-10-616-279-2_COPY_188_210
Perfect score: 121
Sequence: 1 DAGTDSGFTFSSPNFATIPQDTV 23

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	121	100.0	216	2	Q9H7I1_HUMAN	Q9h7i1 homo sapien
2	121	100.0	289	2	Q6KAS6_MOUSE	Q6kas6 mus musculu
3	121	100.0	330	1	SPON2_MOUSE	Q8bms2 mus musculu
4	121	100.0	330	1	SPON2_RAT	Q9wv75 rattus norv

5	121	100.0	330	2	Q8VD28_MOUSE	Q8vd28	mus musculus
6	121	100.0	331	1	SPON2_HUMAN	Q9bud6	homo sapien
7	121	100.0	331	2	Q4W5N4_HUMAN	Q4w5n4	homo sapien
8	121	100.0	331	2	Q5RFG6_PONPY	Q5rfg6	pongo pygma
9	114	94.2	313	2	Q6DCM4_XENLA	Q6dcm4	xenopus lae
10	110	90.9	331	2	O42112_BRARE	O42112	brachydanio
11	109	90.1	355	2	Q4SQV5_TETNG	Q4sqv5	tetraodon n
12	95	78.5	334	2	O42111_BRARE	O42111	brachydanio
13	93	76.9	280	2	Q4SDS0_TETNG	Q4sds0	tetraodon n
14	86	71.1	803	1	SPON1_XENLA	P35447	xenopus lae
15	84	69.4	598	2	O02029_DROME	O02029	drosophila
16	82	67.8	557	2	Q4SPB7_TETNG	Q4spb7	tetraodon n
17	82	67.8	601	2	Q9V746_DROME	Q9v746	drosophila
18	82	67.8	729	2	Q69ZZ7_MOUSE	Q69zz7	mus musculus
19	82	67.8	807	1	SPON1_BOVIN	Q9glx9	bos taurus
20	82	67.8	807	1	SPON1_HUMAN	Q9hcb6	homo sapien
21	82	67.8	807	1	SPON1_MOUSE	Q8vcc9	mus musculus
22	82	67.8	807	1	SPON1_RAT	P35446	rattus norv
23	82	67.8	807	2	Q3B7D6_RAT	Q3b7d6	rattus norv
24	81	66.9	802	1	SPON1_CHICK	Q9w770	gallus gall
25	80	66.1	806	2	Q4SOW9_TETNG	Q4sow9	tetraodon n
26	75	62.0	808	2	O42113_BRARE	O42113	brachydanio
27	74	61.2	803	2	O42114_BRARE	O42114	brachydanio
28	72	59.5	898	2	O76822_BRAFL	O76822	branchiosto
29	67	55.4	819	2	Q19305_CAEEL	Q19305	caenorhabdi
30	67	55.4	820	2	Q61C53_CAEER	Q61c53	caenorhabdi
31	64	52.9	461	2	Q95S22_DROME	Q95s22	drosophila
32	64	52.9	628	2	Q7KRF4_DROME	Q7krf4	drosophila
33	64	52.9	763	2	Q9XZD0_DROME	Q9xzd0	drosophila
34	60	49.6	505	2	Q5TN62_ANOGA	Q5tn62	anopheles g
35	60	49.6	845	2	Q7Q082_ANOGA	Q7q082	anopheles g
36	58	47.9	632	2	Q5TMM3_ANOGA	Q5tmm3	anopheles g
37	58	47.9	781	2	Q7PZ75_ANOGA	Q7pz75	anopheles g
38	55	45.5	549	2	Q8T988_DROME	Q8t988	drosophila
39	55	45.5	839	2	Q8ML26_DROME	Q8ml26	drosophila
40	54	44.6	873	2	Q7KR42_DROME	Q7kr42	drosophila
41	52	43.0	110	2	Q2RS24_RHORU	Q2rs24	rhodospiril
42	52	43.0	661	2	Q7U449_SYNPX	Q7u449	synechococc
43	52	43.0	1521	2	Q8CHS9_MOUSE	Q8chs9	mus musculus
44	52	43.0	2112	2	Q80U93_MOUSE	Q80u93	mus musculus
45	51	42.1	184	2	Q4FXG8_LEIMA	Q4fxg8	leishmania

ALIGNMENTS

RESULT 1

Q9H7I1_HUMAN

ID Q9H7I1_HUMAN PRELIMINARY; PRT; 216 AA.

AC Q9H7I1;

DT 01-MAR-2001, integrated into UniProtKB/TrEMBL.

DT 01-MAR-2001, sequence version 1.

DT 07-FEB-2006, entry version 13.

DE FLJ00108 protein (Fragment).

GN Name=FLJ00108;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;

OC Homo.

OX NCBI_TaxID=9606;

RN [1]

Comments /
Suggestions

Result No.	Score	% Query Match	Length	DB	ID	Description
1	58	100.0	12	4	AAB82476	Aab82476 Human ext
2	58	100.0	12	9	ADW76931	Adw76931 Human RG1
3	58	100.0	249	3	AAB34753	Aab34753 Human sec
4	58	100.0	299	3	AAY73490	Aay73490 Human sec
5	58	100.0	331	2	AAW23663	Aaw23663 Human neu
6	58	100.0	331	2	AAW70589	Aaw70589 Adhesion-
7	58	100.0	331	2	AAW83328	Aaw83328 Human min
8	58	100.0	331	2	AAY41721	Aay41721 Human PRO
9	58	100.0	331	2	AAW92460	Aaw92460 Human NAF
10	58	100.0	331	3	AAB33465	Aab33465 Human PRO
11	58	100.0	331	3	AAY79561	Aay79561 Cancer sp
12	58	100.0	331	3	AAB44277	Aab44277 Human PRO
13	58	100.0	331	3	AAY95349	Aay95349 Human PRO
14	58	100.0	331	4	AAM93266	Aam93266 Human pol
15	58	100.0	331	4	AAM93324	Aam93324 Human pol
16	58	100.0	331	4	AAM38872	Aam38872 Human pol
17	58	100.0	331	4	AAB82472	Aab82472 Human ext
18	58	100.0	331	5	ABG61806	Abg61806 Prostate
19	58	100.0	331	5	AAU79944	Aau79944 Human Spo
20	58	100.0	331	5	ABB77393	Abb77393 Human spo
21	58	100.0	331	5	AAE20463	Aae20463 Human tum
22	58	100.0	331	6	ABO25223	Abo25223 Novel hum
23	58	100.0	331	6	ABU72229	Abu72229 Novel hum
24	58	100.0	331	6	ABU84909	Abu84909 Human sec
25	58	100.0	331	6	ABU61107	Abu61107 Human PRO
26	58	100.0	331	6	ABU80376	Abu80376 Human sec
27	58	100.0	331	6	ABG75949	Abg75949 Human ant
28	58	100.0	331	6	ADA24775	Ada24775 Novel hum
29	58	100.0	331	6	ABO19678	Abo19678 Novel hum
30	58	100.0	331	6	ADA12436	Ada12436 Human sec
31	58	100.0	331	6	ABO19569	Abo19569 Novel hum
32	58	100.0	331	7	ADB73742	Adb73742 Human PRO
33	58	100.0	331	7	ADB76458	Adb76458 Human PRO
34	58	100.0	331	7	ADB75561	Adb75561 Prostate
35	58	100.0	331	7	ADC43884	Adc43884 Human sec
36	58	100.0	331	7	ADC61644	Adc61644 Human sec
37	58	100.0	331	7	ADC63608	Adc63608 Human sec
38	58	100.0	331	7	ADC66708	Adc66708 Human sec
39	58	100.0	331	7	ADC68832	Adc68832 Human sec
40	58	100.0	331	7	ADC62892	Adc62892 Human sec
41	58	100.0	331	7	ADC67957	Adc67957 Human sec
42	58	100.0	331	7	ADC41277	Adc41277 Human sec
43	58	100.0	331	7	ADC67332	Adc67332 Human sec
44	58	100.0	331	7	ADC62268	Adc62268 Human sec
45	58	100.0	331	7	ADC41901	Adc41901 Human sec
46	58	100.0	331	7	ADE49270	Ade49270 Human sec
47	58	100.0	331	7	ADE35324	Ade35324 Human sec
48	58	100.0	331	7	ADE16438	Adel6438 Human sec
49	58	100.0	331	7	ADD73053	Add73053 Human sec
50	58	100.0	331	7	ADD72411	Add72411 Human sec
51	58	100.0	331	7	ADE17062	Adel17062 Human sec
52	58	100.0	331	7	ADF47076	Adf47076 Human sec
53	58	100.0	331	7	ADG42579	Adg42579 Novel hum
54	58	100.0	331	7	ADG42585	Adg42585 Human ext
55	58	100.0	331	7	ADG42586	Adg42586 Human ext
56	58	100.0	331	7	ADG42587	Adg42587 Human ext
57	58	100.0	331	7	ADG52833	Adg52833 Human sec

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OM protein - protein search, using sw model

Run on: May 25, 2006, 12:44:44 ; Search time 24.7826 Seconds
(without alignments)
42.383 Million cell updates/sec

Title: US-10-616-279-2_COPY_263_274
Perfect score: 58
Sequence: 1 NEIVDSASVPET 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Issued_Patents_AA:*
1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query	
No.	Score	Match Length DB ID Description

1	58	100.0	12	2	US-09-732-357B-12	Sequence 12, Appl
2	58	100.0	299	2	US-09-311-021-202	Sequence 202, App
3	58	100.0	331	1	US-08-799-173A-2	Sequence 2, Appli
4	58	100.0	331	2	US-09-732-357B-2	Sequence 2, Appli
5	58	100.0	331	2	US-09-170-042A-2	Sequence 2, Appli
6	58	100.0	331	2	US-09-949-002-397	Sequence 397, App
7	58	100.0	331	2	US-09-999-833A-236	Sequence 236, App
8	58	100.0	331	2	US-09-807-200-2	Sequence 2, Appli
9	58	100.0	331	2	US-10-020-445A-236	Sequence 236, App
10	58	100.0	331	2	US-09-978-189-236	Sequence 236, App
11	58	100.0	331	2	US-10-017-085A-236	Sequence 236, App
12	58	100.0	331	3	US-10-145-129A-236	Sequence 236, App
13	58	100.0	331	3	US-10-013-929A-236	Sequence 236, App
14	58	100.0	331	3	US-10-013-917A-236	Sequence 236, App
15	58	100.0	422	2	US-09-949-002-504	Sequence 504, App
16	53	91.4	330	2	US-09-732-357B-13	Sequence 13, Appl
17	50	86.2	37	2	US-09-022-238-3	Sequence 3, Appli
18	50	86.2	37	2	US-09-371-696-3	Sequence 3, Appli
19	50	86.2	132	2	US-09-022-238-2	Sequence 2, Appli
20	50	86.2	330	2	US-09-371-696-2	Sequence 2, Appli
21	37	63.8	717	1	US-08-435-925C-2	Sequence 2, Appli
22	37	63.8	749	2	US-09-562-737-96	Sequence 96, Appl
23	36	62.1	141	2	US-09-270-767-45511	Sequence 45511, A
24	36	62.1	190	2	US-09-605-703B-2504	Sequence 2504, Ap
25	36	62.1	256	2	US-09-305-489-2	Sequence 2, Appli
26	36	62.1	408	2	US-09-252-991A-33131	Sequence 33131, A
27	36	62.1	2216	2	US-09-902-540-12221	Sequence 12221, A
28	35	60.3	70	2	US-09-252-991A-26553	Sequence 26553, A
29	35	60.3	297	2	US-09-252-991A-28307	Sequence 28307, A
30	35	60.3	578	2	US-09-949-016-6715	Sequence 6715, Ap
31	35	60.3	583	2	US-09-949-016-9840	Sequence 9840, Ap
32	35	60.3	904	2	US-09-543-681A-6943	Sequence 6943, Ap
33	34	58.6	127	2	US-09-270-767-42359	Sequence 42359, A
34	34	58.6	161	2	US-09-107-532A-6131	Sequence 6131, Ap
35	34	58.6	178	2	US-09-540-236-2174	Sequence 2174, Ap
36	34	58.6	188	2	US-09-252-991A-18537	Sequence 18537, A
37	34	58.6	241	2	US-09-825-414-22	Sequence 22, Appl
38	34	58.6	360	2	US-09-252-991A-26691	Sequence 26691, A
39	34	58.6	474	2	US-09-732-615-12	Sequence 12, Appl
40	34	58.6	474	2	US-10-273-051-12	Sequence 12, Appl
41	34	58.6	826	2	US-09-830-762-5	Sequence 5, Appli
42	34	58.6	854	2	US-09-830-762-2	Sequence 2, Appli
43	33	56.9	154	2	US-09-270-767-57940	Sequence 57940, A
44	33	56.9	189	2	US-09-605-703B-1300	Sequence 1300, Ap
45	33	56.9	195	2	US-09-248-796A-27805	Sequence 27805, A
46	33	56.9	205	2	US-09-252-991A-24792	Sequence 24792, A
47	33	56.9	232	1	US-08-956-047-36	Sequence 36, Appl
48	33	56.9	252	5	PCT-US96-01314-56	Sequence 56, Appl
49	33	56.9	271	5	PCT-US95-02455-2	Sequence 2, Appli
50	33	56.9	273	2	US-09-248-796A-15037	Sequence 15037, A
51	33	56.9	312	2	US-09-475-316A-64	Sequence 64, Appl
52	33	56.9	312	2	US-09-704-640-64	Sequence 64, Appl
53	33	56.9	429	1	US-08-745-977-4	Sequence 4, Appli
54	33	56.9	429	2	US-09-040-699A-4	Sequence 4, Appli
55	33	56.9	532	2	US-09-270-767-46369	Sequence 46369, A
56	33	56.9	643	2	US-09-178-252-25	Sequence 25, Appl
57	33	56.9	643	2	US-09-826-660-25	Sequence 25, Appl
58	33	56.9	653	2	US-09-661-322A-6	Sequence 6, Appli
59	33	56.9	799	2	US-10-094-749-1917	Sequence 1917, Ap
60	33	56.9	1186	2	US-09-178-252-23	Sequence 23, Appl
61	33	56.9	1186	2	US-09-826-660-23	Sequence 23, Appl

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OM protein - protein search, using sw model

Run on: May 25, 2006, 13:06:00 ; Search time 5.21739 Seconds
(without alignments)
25.616 Million cell updates/sec

Title: US-10-616-279-2_COPY_263_274
Perfect score: 58
Sequence: 1 NEIVDSASVPET 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 56051 seqs, 11137335 residues

Total number of hits satisfying chosen parameters: 56051

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Published_Applications_AA_New:*
1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
8: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result %
Query

No.	Score	Match	Length	DB	ID	Description
1	36	62.1	19	7	US-11-122-986-686	Sequence 686, App
2	36	62.1	464	7	US-11-122-986-239	Sequence 239, App
3	36	62.1	464	7	US-11-122-986-241	Sequence 241, App
4	33	56.9	192	6	US-10-953-349-36740	Sequence 36740, A
5	33	56.9	205	6	US-10-953-349-36739	Sequence 36739, A
6	33	56.9	257	6	US-10-953-349-36738	Sequence 36738, A
7	33	56.9	304	6	US-10-953-349-6569	Sequence 6569, Ap
8	33	56.9	324	6	US-10-953-349-11519	Sequence 11519, A
9	33	56.9	340	6	US-10-953-349-28435	Sequence 28435, A
10	33	56.9	360	6	US-10-953-349-6568	Sequence 6568, Ap
11	33	56.9	366	6	US-10-953-349-28434	Sequence 28434, A
12	33	56.9	397	6	US-10-953-349-6567	Sequence 6567, Ap
13	33	56.9	1822	6	US-10-505-928-700	Sequence 700, App
14	32	55.2	361	6	US-10-953-349-707	Sequence 707, App
15	32	55.2	373	6	US-10-953-349-706	Sequence 706, App
16	32	55.2	396	6	US-10-953-349-4090	Sequence 4090, Ap
17	32	55.2	421	6	US-10-953-349-4089	Sequence 4089, Ap
18	32	55.2	580	6	US-10-953-349-12416	Sequence 12416, A
19	32	55.2	619	6	US-10-953-349-12415	Sequence 12415, A
20	32	55.2	621	6	US-10-953-349-12414	Sequence 12414, A
21	31	53.4	198	6	US-10-953-349-26364	Sequence 26364, A
22	31	53.4	222	7	US-11-293-697-4522	Sequence 4522, Ap
23	31	53.4	242	6	US-10-953-349-26363	Sequence 26363, A
24	31	53.4	253	7	US-11-293-697-4349	Sequence 4349, Ap
25	31	53.4	255	6	US-10-953-349-38691	Sequence 38691, A
26	31	53.4	310	6	US-10-953-349-38690	Sequence 38690, A
27	31	53.4	325	6	US-10-953-349-38689	Sequence 38689, A
28	31	53.4	495	6	US-10-953-349-22310	Sequence 22310, A
29	31	53.4	580	6	US-10-953-349-1290	Sequence 1290, Ap
30	31	53.4	737	6	US-10-953-349-1289	Sequence 1289, Ap
31	31	53.4	870	6	US-10-953-349-1288	Sequence 1288, Ap
32	30	51.7	68	6	US-10-953-349-27055	Sequence 27055, A
33	30	51.7	95	6	US-10-953-349-18359	Sequence 18359, A
34	30	51.7	105	6	US-10-953-349-4253	Sequence 4253, Ap
35	30	51.7	105	6	US-10-953-349-6846	Sequence 6846, Ap
36	30	51.7	120	7	US-11-293-697-4269	Sequence 4269, Ap
37	30	51.7	135	6	US-10-953-349-4252	Sequence 4252, Ap
38	30	51.7	135	6	US-10-953-349-6845	Sequence 6845, Ap
39	30	51.7	142	6	US-10-953-349-18358	Sequence 18358, A
40	30	51.7	171	6	US-10-953-349-18357	Sequence 18357, A
41	30	51.7	186	6	US-10-953-349-4251	Sequence 4251, Ap
42	30	51.7	186	6	US-10-953-349-6844	Sequence 6844, Ap
43	30	51.7	221	6	US-10-953-349-17730	Sequence 17730, A
44	30	51.7	275	6	US-10-953-349-24566	Sequence 24566, A
45	30	51.7	277	6	US-10-953-349-17729	Sequence 17729, A
46	30	51.7	279	6	US-10-953-349-19383	Sequence 19383, A
47	30	51.7	317	6	US-10-953-349-24565	Sequence 24565, A
48	30	51.7	322	6	US-10-953-349-17728	Sequence 17728, A
49	30	51.7	354	6	US-10-953-349-23264	Sequence 23264, A
50	30	51.7	401	6	US-10-953-349-24564	Sequence 24564, A
51	30	51.7	415	6	US-10-953-349-4574	Sequence 4574, Ap
52	30	51.7	419	6	US-10-953-349-6306	Sequence 6306, Ap
53	30	51.7	511	7	US-11-121-154-96	Sequence 96, Appl
54	30	51.7	515	6	US-10-953-349-6305	Sequence 6305, Ap
55	30	51.7	517	6	US-10-953-349-4573	Sequence 4573, Ap
56	30	51.7	540	6	US-10-953-349-6304	Sequence 6304, Ap
57	30	51.7	553	6	US-10-953-349-4572	Sequence 4572, Ap
58	29	50.0	64	6	US-10-953-349-9704	Sequence 9704, Ap
59	29	50.0	71	6	US-10-953-349-38080	Sequence 38080, A

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OM protein - protein search, using sw model

Run on: May 25, 2006, 13:05:59 ; Search time 86.6087 Seconds
(without alignments)
64.180 Million cell updates/sec

Title: US-10-616-279-2_COPY_263_274
Perfect score: 58
Sequence: 1 NEIVDSASVPET 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Published_Applications_AA_Main:*

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- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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No.		%				

1	58	100.0	12	3	US-09-732-357A-12	Sequence 12, Appl
2	58	100.0	12	4	US-10-616-279-12	Sequence 12, Appl
3	58	100.0	12	4	US-10-624-884-12	Sequence 12, Appl
4	58	100.0	12	5	US-10-895-183-12	Sequence 12, Appl
5	58	100.0	331	3	US-09-732-357A-2	Sequence 2, Appli
6	58	100.0	331	3	US-09-978-295A-236	Sequence 236, App
7	58	100.0	331	3	US-09-938-418-8	Sequence 8, Appli
8	58	100.0	331	3	US-09-978-697-236	Sequence 236, App
9	58	100.0	331	3	US-09-978-192A-236	Sequence 236, App
10	58	100.0	331	3	US-09-999-832A-236	Sequence 236, App
11	58	100.0	331	3	US-09-978-189-236	Sequence 236, App
12	58	100.0	331	3	US-09-978-608A-236	Sequence 236, App
13	58	100.0	331	3	US-09-978-585A-236	Sequence 236, App
14	58	100.0	331	3	US-09-978-191A-236	Sequence 236, App
15	58	100.0	331	3	US-09-978-403A-236	Sequence 236, App
16	58	100.0	331	3	US-09-978-564A-236	Sequence 236, App
17	58	100.0	331	3	US-09-999-833A-236	Sequence 236, App
18	58	100.0	331	3	US-09-981-915A-236	Sequence 236, App
19	58	100.0	331	3	US-09-978-824-236	Sequence 236, App
20	58	100.0	331	3	US-09-918-585A-236	Sequence 236, App
21	58	100.0	331	3	US-09-999-834A-236	Sequence 236, App
22	58	100.0	331	3	US-09-978-423A-236	Sequence 236, App
23	58	100.0	331	3	US-09-978-193A-236	Sequence 236, App
24	58	100.0	331	3	US-09-999-830A-236	Sequence 236, App
25	58	100.0	331	3	US-09-978-757A-236	Sequence 236, App
26	58	100.0	331	3	US-09-978-187B-236	Sequence 236, App
27	58	100.0	331	3	US-09-978-643A-236	Sequence 236, App
28	58	100.0	331	3	US-09-978-375A-236	Sequence 236, App
29	58	100.0	331	3	US-09-978-298A-236	Sequence 236, App
30	58	100.0	331	3	US-09-978-188A-236	Sequence 236, App
31	58	100.0	331	3	US-09-978-681A-236	Sequence 236, App
32	58	100.0	331	3	US-09-978-194A-236	Sequence 236, App
33	58	100.0	331	3	US-09-999-829A-236	Sequence 236, App
34	58	100.0	331	3	US-09-978-299A-236	Sequence 236, App
35	58	100.0	331	3	US-09-978-544A-236	Sequence 236, App
36	58	100.0	331	3	US-09-978-665A-236	Sequence 236, App
37	58	100.0	331	3	US-09-978-802A-236	Sequence 236, App
38	58	100.0	331	3	US-09-970-944-12	Sequence 12, Appl
39	58	100.0	331	3	US-09-970-944-38	Sequence 38, Appl
40	58	100.0	331	3	US-09-970-944-39	Sequence 39, Appl
41	58	100.0	331	3	US-09-970-944-40	Sequence 40, Appl
42	58	100.0	331	3	US-09-999-831A-236	Sequence 236, App
43	58	100.0	331	3	US-09-978-824-236	Sequence 236, App
44	58	100.0	331	4	US-10-017-081A-236	Sequence 236, App
45	58	100.0	331	4	US-10-167-749-236	Sequence 236, App
46	58	100.0	331	4	US-10-013-921A-236	Sequence 236, App
47	58	100.0	331	4	US-10-013-929A-236	Sequence 236, App
48	58	100.0	331	4	US-10-016-177A-236	Sequence 236, App
49	58	100.0	331	4	US-10-166-709A-236	Sequence 236, App
50	58	100.0	331	4	US-10-205-823-385	Sequence 385, App
51	58	100.0	331	4	US-10-143-031A-236	Sequence 236, App
52	58	100.0	331	4	US-10-143-030A-236	Sequence 236, App
53	58	100.0	331	4	US-10-002-967A-236	Sequence 236, App
54	58	100.0	331	4	US-10-017-083A-236	Sequence 236, App
55	58	100.0	331	4	US-10-145-128A-236	Sequence 236, App
56	58	100.0	331	4	US-10-017-191A-236	Sequence 236, App
57	58	100.0	331	4	US-10-143-028A-236	Sequence 236, App
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60	58	100.0	331	4	US-10-165-067A-236	Sequence 236, App
61	58	100.0	331	4	US-10-145-017A-236	Sequence 236, App

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A;Cross-references: UNIPROT:O83326; UNIPARC:UPI00001395DB; GB:AE001210; GB:AE000520; T14850 S-layer protein precursor - *Bacillus stearothermophilus* C;Species: *Bacillus stearothermophilus* C;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-1099 / NPMVDSAATPNT 809 RESULT 8 AC1448 gp19 (Bacteriophage A118) homolog lin0122 [imported] - Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; Garcia-Del Portillo, F.; Garrido, P.; Gautier, L.; C P. A;Title: Comparative genomics of *Listeria* species. A;Reference number: AB1077; MUID:215372 Matches 9; Conservative 2; Mismatches 1; Indels 3; Gaps 1; Qy 1 NEIVD---SASVPET 12 ||:||| || Kowalik, D.J.; Lagrou, M.; Garber, R.L.; Goltry, L.; Tolentino, E.; Westbrook-Wadman, S.; Yuan, Y. A83371 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-194 A;Cross-references: UNIPROT:NEILQSAGVPK 41 RESULT 10 G89899 undecaprenyl pyrophosphatase synthetase [imported] - Sta N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; Hirakawa, H.; Kuhara, S.; Goto, S.; Yabuzaki, I. references: UNIPROT:P60477; UNIPARC:UPI00000CA967; GB:BA000018; PID:g13701060; PIDN:EB [imported] - *Mycobacterium leprae* C;Species: *Mycobacterium leprae* C;Date: 20-Apr-2001 #sequence Moule, S.; Murphy, L.; Oliver, K.; Quail, M.A.; Rajandream, M.A.; Rutherford, K.M. Nature 409, 100 UNIPROT:Q9CD96; UNIPARC:UPI00000C6C46; GB:AL450380; NID:g13092498; PIDN:CAC29626.1 (strain PCC 7120) C;Species: *Nostoc* sp. PCC 7120 A;Note: *Nostoc* sp. strain PCC 7120 is a synonym M.; Yasuda, M.; Tabata, S. DNA Res. 8, 205-213, 2001 A;Title: Complete Genomic Sequence of the C;Genetics: A;Gene: all1325 Query Match 62.1%; Score 36; DB 2; Length 372; Best Local Similarity December 1996 A;Description: The sequence of *C. elegans* cosmid C32B5. A;Reference number: Z 62.1%; Score 36; DB 2; Length 392; Best Local Similarity 60.0%; Pred. No. 44; Matches 6; Conservative Warrener, P.; Hickey, M.J.; Brinkman, F.S.L.; Hufnagle, W.O.; Kowalik, D.J.; Lagrou, M.; Garber, R. A82950; MUID:20437337; PMID:10984043 A;Accession: E83029 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-980 A;Cross-references: UNIPROT:Q08972; UNIPARC:UPI0000053084; EMBL:Z73582; NID:g1370467; PIDN:CA R;Urrestarazu, L.A. submitted to the EMBL Data Library, December 1995 A;Reference number: S61 nucleotide-binding motif A (P-loop) F;829-1105/Domain: ATP-binding cassette homology F;846-85 C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004 C;Accession: G Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E. Nature 390, 249-256, 1997 A;A Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, S. A;Authors: Lauber, J.; Lazarevic, V.; Sadaie, Y.; Sato, T.; Scanlon, E. A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J. Yoshida, K. A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A. A;Title: The con PID:g2634346 A;Experimental source: strain 168 C;Genetics: A;Gene: yodB C;Superfamily: conse #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004 C;Accession: A72310 R;Nelson, K.E.; A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome sequence of C;Superfamily: *Thermotoga maritima* hypothetical protein TM0980 Query Match 60.3%; Score 35; E89813 R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguchi A;Title: Whole genome sequencing of methicillin-resistant *Staphylococcus aureus*. A;Reference number: 54.5%; Pred. No. 40; Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0; Qy 1 NEIVDSA Hufnagle, W.O.; Kowalik, D.J.; Lagrou, M.; Garber, R.L.; Goltry, L.; Tolentino, E.; Westbrook-Wadman A;Accession: G83131 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-259 A;Cross-refer

Mismatches 1; Indels 0; Gaps 0; Qy 3 IVDSASVPE 11 |||:| ||| Db 158 IVDAAEVPE 166 RESULT 22 and legumes. A;Reference number: Z14734; MUID:97305956; PMID:9163424 A;Accession: T4706 VDSASVPET 12 || |:|:| Db 83 VDGASIPQT 91 RESULT 23 S04718 DNA-directed RNA polymerase (RNA polymerase of the archaebacterium *Sulfolobus acidocaldarius*. A;Reference number: S04714; F.; Garrett, R.A.; Zillig, W. Proc. Natl. Acad. Sci. U.S.A. 86, 4569-4573, 1989 A;Title: Archaebacter C;Genetics: A;Gene: rpoC C;Function: A;Description: (EC 2.7.7.6) [validated, MUID:89315197] C; *Sulfolobus solfataricus* C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 15- Gaasterland, T.; Garrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J. submitted to GenBank DB 2; Length 395; Best Local Similarity 63.6%; Pred. No. 71; Matches 7; Conservative 1; Mismatch M.; James, K.D.; Churcher, C.; Mungall, K.L.; Baker, S.; Basham, D.; Bentley, S.D.; Brooks, K.; C number: AB0001; MUID:21470413; PMID:11586360 A;Accession: AF0350 A;Status: preliminary A Conservative 3; Mismatches 2; Indels 0; Gaps 0; Qy 2 EIVDSASVPET 12 |:| ||:| | Db 242 ELLDKA K. Nucleic Acids Res. 28, 4317-4331, 2000 A;Title: Complete genome sequence of the alkaliphilic b source: strain C-125 C;Genetics: A;Gene: dacA C;Superfamily: penicillin-binding protein 5 Query M #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004 C;Accession: S54025; S28567 R;Lye Library, November 1992 A;Description: MSS1 a nuclear-encoded mitochondrial GTPase involved in 13R A;Genome: nuclear C;Superfamily: thiophen / furan oxidation protein; translation elongation f NEIVDSASVP 10 | :|||:| Db 67 NRLVDSSTVP 76 RESULT 28 F86648 hypothetical protein ybjJ [im bacterium *Lactococcus lactis* ssp. *lactis* IL1403. A;Reference number: A86625; MUID:21235186; P Length 535; Best Local Similarity 50.0%; Pred. No. 1e+02; Matches 5; Conservative 5; Mismatch T20445 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 624; Best Local Similarity 60.0%; Pred. No. 1.2e+02; Matches 6; Conservative 2; Mismatches 2; I C.L.; Brooks, S.Y.; Buehler, E.; Chan, A.; Chao, Q.; Chen, H.; Cheuk, R.F.; Chin, C.W.; Chung, M. Lee, A.; Lee, J.M.; Lenz, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Ma Davis, R.W. A;Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*. A;Reference Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0; Qy 2 EIVDSASVPET 12 ::| |:|:| Db E.; Chan, A.; Chao, Q.; Chen, H.; Cheuk, R.F.; Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; (Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, A.; Militscher, J.; Mirandi and analysis of chromosome 1 of the plant *Arabidopsis*. A;Reference number: A86141; MUID:2101 Conservative 2; Mismatches 4; Indels 0; Gaps 0; Qy 1 NEIVDSASVPET 12 | : : |||| Db 676 NSVAE Protein Sequence Database, November 1999 A;Reference number: Z23023 A;Accession: T46116 A 1229; Best Local Similarity 80.0%; Pred. No. 2.6e+02; Matches 8; Conservative 0; Mismatches 2; C1orf9 gene encodes a putative transmembrane member of a novel protein family. A;Reference nu Length 1254; Best Local Similarity 66.7%; Pred. No. 2.6e+02; Matches 6; Conservative 3; Mismatch A;Description: Molecular cloning and tissue-specific expression of the mutator2 gene (*mu2*) in *Dros* 60.3%; Score 35; DB 2; Length 1261; Best Local Similarity 58.3%; Pred. No. 2.6e+02; Matches 7, heterodimeric coiled-coil protein required for mitotic chromosome condensation in vitro. A;Referenc 60.3%; Score 35; DB 2; Length 1290; Best Local Similarity 63.6%; Pred. No. 2.7e+02; Matches 7, Warrenner, P.; Hickey, M.J.; Brinkman, F.S.L.; Hufnagle, W.O.; Kowalik, D.J.; Lagrou, M.; Garber, R A82950; MUID:20437337; PMID:10984043 A;Accession: C83269 A;Status: preliminary A;Molecule Gaps 0; Qy 2 EIVDSASVPET 12 |:|: || ||| Db 93 ELVELASQPET 103 RESULT 37 D87150 polypeptide K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd, S.; Hornsby, T.; Jagels, K.; Lacroix, C PMID:11234002 A;Accession: D87150 A;Status: preliminary A;Molecule type: DNA A;Residues: 1- NPILETSEIPET 95 RESULT 38 T21655 hypothetical protein F32D8.5a - *Caenorhabditis elegans* C;Sp UNIPARC:UPI0000077CDE; EMBL:Z74031; PIDN:CAA98457.1; GSPDB:GN00023; CESP:F32D8.5a , *Methanobacterium thermoautotrophicum* (strain Delta H) C;Species: *Methanobacterium thermoaut* A.; Bush, D.; Safer, H.; Patwell, D.; Prabhakar, S.; McDougall, S.; Shimer, G.; Goyal, A.; Pietrovkov shown A;Molecule type: DNA A;Residues: 1-226 A;Cross-references: UNIPROT:O26767; UNIPARC: hypothetical protein F32D8.5b - *Caenorhabditis elegans* C;Species: *Caenorhabditis elegans* C;Date GSPDB:GN00023; CESP:F32D8.5b A;Experimental source: clone F32D8 C;Genetics: A;Gene: CESP A;Note: *Nostoc* sp. strain PCC 7120 is a synonym of *Anabaena* sp. strain PCC 7120 C;Date: 14-Dec 2001 A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium *Ana* Score 34; DB 2; Length 291; Best Local Similarity 66.7%; Pred. No. 79; Matches 6; Conservative 2 Alonso, J.; Altaf, H.; Araujo, R.; Bowman, C.L.; Brooks, S.Y.; Buehler, E.; Chan, A.; Chao, Q.; Che D.B.; Kwan, A.; Lam, B.; Langin-Hooper, S.; Lee, A.; Lee, J.M.; Lenz, C.A.; Li, J.H.; Li, Y.; Lin, X.;

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OM protein - protein search, using sw model

Run on: May 25, 2006, 12:28:34 ; Search time 123.13 Seconds
(without alignments)
90.150 Million cell updates/sec

Title: US-10-616-279-2_COPY_263_274
Perfect score: 58
Sequence: 1 NEIVDSASVPET 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : UniProt_7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	58	100.0	331	1	SPON2_HUMAN	Q9bud6 homo sapien
2	58	100.0	331	2	Q4W5N4_HUMAN	Q4w5n4 homo sapien
3	58	100.0	331	2	Q5RFG6_PONPY	Q5rfg6 pongo pygma
4	53	91.4	129	2	Q3TEM5_MOUSE	Q3tem5 mus musculu

5	53	91.4	289	2	Q6KAS6_MOUSE	Q6kas6	mus musculu
6	53	91.4	330	1	SPON2_MOUSE	Q8bms2	mus musculu
7	53	91.4	330	1	SPON2_RAT	Q9wv75	rattus norv
8	53	91.4	330	2	Q8VD28_MOUSE	Q8vd28	mus musculu
9	41	70.7	637	2	Q4ZN61_PSEU2	Q4zn61	pseudomonas
10	40	69.0	304	2	Q58Z28_LACRH	Q58z28	lactobacill
11	40	69.0	429	2	Q5WM20_BACSK	Q5wm20	bacillus cl
12	40	69.0	999	2	Q4Q5S1_LEIMA	Q4q5s1	leishmania
13	39	67.2	157	2	Q8DTK7_STRMU	Q8dtk7	streptococc
14	39	67.2	242	2	Q94MR8_9CAUD	Q94mr8	bacterioph
15	39	67.2	304	2	Q58Z11_LACRH	Q58z11	lactobacill
16	39	67.2	651	2	Q3UTY5_MOUSE	Q3uty5	mus musculu
17	39	67.2	680	2	Q8JZW6_MOUSE	Q8jzw6	mus musculu
18	39	67.2	681	2	Q3UWJ5_MOUSE	Q3uwj5	mus musculu
19	39	67.2	776	2	Q7VH62_HELHP	Q7vh62	helicobacte
20	39	67.2	972	2	Q8CDM3_MOUSE	Q8cdm3	mus musculu
21	39	67.2	1001	1	RPGR_MOUSE	Q9r0x5	mus musculu
22	38	65.5	226	2	Q5C6R8_SCHJA	Q5c6r8	schistosoma
23	38	65.5	323	2	Q6AAP3_PROAC	Q6aap3	propionibac
24	38	65.5	370	2	Q754K6_ASHGO	Q754k6	ashbya goss
25	38	65.5	440	2	Q39AG5_BURS3	Q39ag5	burkholderi
26	38	65.5	441	2	Q7MUI5_PORGI	Q7mui5	porphyromon
27	38	65.5	537	2	Q7UXT4_RHOBA	Q7uxt4	rhodopirell
28	38	65.5	928	2	Q8H7U0_ORYSA	Q8h7u0	oryza sativ
29	38	65.5	1102	1	RPOB_SYNY3	P77965	synechocyst
30	38	65.5	1736	2	Q9C2J9_NEUCR	Q9c2j9	neurospora
31	37	63.8	210	2	Q4HJ72_CAMLA	Q4hj72	campylobact
32	37	63.8	221	2	Q62PK9_BACLD	Q62pk9	bacillus li
33	37	63.8	222	2	Q65E37_BACLD	Q65e37	bacillus li
34	37	63.8	271	2	Q4Q7J3_LEIMA	Q4q7j3	leishmania
35	37	63.8	287	1	H1_LYCES	P37218	lycopersico
36	37	63.8	339	2	Q62IN2_BURMA	Q62in2	burkholderi
37	37	63.8	339	2	Q63VN6_BURPS	Q63vn6	burkholderi
38	37	63.8	360	2	Q3JUB2_BURP1	Q3jub2	burkholderi
39	37	63.8	365	2	Q6BMR8_DEBHA	Q6bmr8	debaryomyce
40	37	63.8	395	2	Q8Y3L1_LISMO	Q8y3l1	listeria mo
41	37	63.8	395	2	Q926T4_LISIN	Q926t4	listeria in
42	37	63.8	403	2	Q4EH56_LISMO	Q4eh56	listeria mo
43	37	63.8	403	2	Q4ET80_LISMO	Q4et80	listeria mo
44	37	63.8	403	2	Q71VT7_LISMF	Q71vt7	listeria mo
45	37	63.8	404	2	Q65NV4_BACLD	Q65nv4	bacillus li
46	37	63.8	446	2	Q3RPS7_RALME	Q3rps7	ralstonia m
47	37	63.8	471	2	Q2X1V8_9GAMM	Q2x1v8	shewanella
48	37	63.8	471	2	Q2ZMR5_SHEPU	Q2zmr5	shewanella
49	37	63.8	512	2	Q7PV52_ANOGA	Q7pv52	anopheles g
50	37	63.8	526	2	Q3E6N1_CHLAU	Q3e6n1	chloroflexu
51	37	63.8	549	2	Q4QBQ6_LEIMA	Q4qbq6	leishmania
52	37	63.8	570	2	Q6JU00_BRARE	Q6juu0	brachydanio
53	37	63.8	570	2	Q6NW58_BRARE	Q6nw58	brachydanio
54	37	63.8	578	2	Q4I1N5_GIBZE	Q4iln5	gibberella
55	37	63.8	593	2	Q3APX5_CHLCH	Q3apx5	chlorobium
56	37	63.8	608	2	Q582I4_9TRYP	Q582i4	trypanosoma
57	37	63.8	653	2	Q5LS11_SILPO	Q5ls11	silicibacte
58	37	63.8	766	2	Q7RI66_PLAYO	Q7ri66	plasmodium
59	37	63.8	810	2	Q5AZL4_EMENI	Q5azl4	aspergillus
60	37	63.8	1039	1	Y304_TREPA	O83326	treponema p
61	37	63.8	1099	2	O68840_BACST	O68840	bacillus st
62	37	63.8	1157	2	Q7RQN5_PLAYO	Q7rqn5	plasmodium
63	37	63.8	1928	2	Q6VZJ3_CNPV	Q6vzj3	canarypox v
64	37	63.8	3971	2	Q6VMD5_9CORO	Q6vmd5	infectious
65	37	63.8	6646	2	Q6VMD6_9CORO	Q6vmd6	infectious

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OM protein - protein search, using sw model

Run on: May 25, 2006, 12:28:19 ; Search time 152.413 Seconds
(without alignments)
56.997 Million cell updates/sec

Title: US-10-616-279-2_COPY_28_46
Perfect score: 99
Sequence: 1 PLGGESICSAGAPAKYSIT 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : A_Geneseq_8:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	99	100.0	19	4	AAB82473	Aab82473 Human ext
2	99	100.0	19	9	ADW76927	Adw76927 Human RG1
3	99	100.0	105	3	AAB34693	Aab34693 Human sec
4	99	100.0	331	4	AAB82472	Aab82472 Human ext
5	99	100.0	331	9	ADW76921	Adw76921 Human RG1
6	91	91.9	290	8	ADT50847	Adt50847 Cancer re
7	91	91.9	298	8	ADT50840	Adt50840 Cancer re
8	91	91.9	330	4	AAE12304	Aae12304 Human NPG
9	91	91.9	331	2	AAW70589	Aaw70589 Adhesion-
10	91	91.9	331	2	AAV41721	Aay41721 Human PRO
11	91	91.9	331	3	AAB33465	Aab33465 Human PRO
12	91	91.9	331	3	AAV79561	Aay79561 Cancer sp
13	91	91.9	331	3	AAB44277	Aab44277 Human PRO
14	91	91.9	331	3	AAV95349	Aay95349 Human PRO
15	91	91.9	331	4	AAM93266	Aam93266 Human pol
16	91	91.9	331	4	AAM93324	Aam93324 Human pol
17	91	91.9	331	4	AAM38872	Aam38872 Human pol
18	91	91.9	331	5	ABG61806	Abg61806 Prostate
19	91	91.9	331	5	AAU79944	Aau79944 Human Spo
20	91	91.9	331	5	ABB77393	Abb77393 Human spo
21	91	91.9	331	5	AAE20463	Aae20463 Human tum
22	91	91.9	331	6	ABO25223	Abo25223 Novel hum
23	91	91.9	331	6	ABU72229	Abu72229 Novel hum
24	91	91.9	331	6	ABU84909	Abu84909 Human sec
25	91	91.9	331	6	ABU61107	Abu61107 Human PRO
26	91	91.9	331	6	ABU80376	Abu80376 Human sec
27	91	91.9	331	6	ABG75949	Abg75949 Human ant
28	91	91.9	331	6	ADA24775	Ada24775 Novel hum
29	91	91.9	331	6	ABO19678	Abo19678 Novel hum
30	91	91.9	331	6	ADA12436	Ada12436 Human sec
31	91	91.9	331	6	ABO19569	Abo19569 Novel hum
32	91	91.9	331	7	ADB73742	Adb73742 Human PRO
33	91	91.9	331	7	ADB76458	Adb76458 Human PRO
34	91	91.9	331	7	ADB75561	Adb75561 Prostate
35	91	91.9	331	7	ADC43884	Adc43884 Human sec
36	91	91.9	331	7	ADC61644	Adc61644 Human sec
37	91	91.9	331	7	ADC63608	Adc63608 Human sec
38	91	91.9	331	7	ADC66708	Adc66708 Human sec
39	91	91.9	331	7	ADC68832	Adc68832 Human sec
40	91	91.9	331	7	ADC62892	Adc62892 Human sec
41	91	91.9	331	7	ADC67957	Adc67957 Human sec
42	91	91.9	331	7	ADC41277	Adc41277 Human sec
43	91	91.9	331	7	ADC67332	Adc67332 Human sec
44	91	91.9	331	7	ADC62268	Adc62268 Human sec
45	91	91.9	331	7	ADC41901	Adc41901 Human sec
46	91	91.9	331	7	ADE49270	Ade49270 Human sec
47	91	91.9	331	7	ADE35324	Ade35324 Human sec
48	91	91.9	331	7	ADE16438	Ade16438 Human sec
49	91	91.9	331	7	ADD73053	Add73053 Human sec
50	91	91.9	331	7	ADD72411	Add72411 Human sec
51	91	91.9	331	7	ADE17062	Ade17062 Human sec
52	91	91.9	331	7	ADF47076	Adf47076 Human sec
53	91	91.9	331	7	ADG42579	Adg42579 Novel hum
54	91	91.9	331	7	ADG42585	Adg42585 Human ext
55	91	91.9	331	7	ADG42587	Adg42587 Human ext
56	91	91.9	331	7	ADG52833	Adg52833 Human sec
57	91	91.9	331	7	ADG60153	Adg60153 Human sec

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OM protein - protein search, using sw model

Run on: May 25, 2006, 12:44:44 ; Search time 39.2391 Seconds
(without alignments)
42.383 Million cell updates/sec

Title: US-10-616-279-2_COPY_28_46
Perfect score: 99
Sequence: 1 PLGGESICSAGAPAKYSIT 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Issued Patents_AA:*
1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query					
No.	Score	Match	Length	ID		Description

1	99	100.0	19	2	US-09-732-357B-8	Sequence 8, Appli
2	99	100.0	331	2	US-09-732-357B-2	Sequence 2, Appli
3	91	91.9	330	2	US-09-371-696-2	Sequence 2, Appli
4	91	91.9	331	2	US-09-949-002-397	Sequence 397, App
5	91	91.9	331	2	US-09-999-833A-236	Sequence 236, App
6	91	91.9	331	2	US-09-807-200-2	Sequence 2, Appli
7	91	91.9	331	2	US-10-020-445A-236	Sequence 236, App
8	91	91.9	331	2	US-09-978-189-236	Sequence 236, App
9	91	91.9	331	2	US-10-017-085A-236	Sequence 236, App
10	91	91.9	331	3	US-10-145-129A-236	Sequence 236, App
11	91	91.9	331	3	US-10-013-929A-236	Sequence 236, App
12	91	91.9	331	3	US-10-013-917A-236	Sequence 236, App
13	91	91.9	422	2	US-09-949-002-504	Sequence 504, App
14	81	81.8	331	1	US-08-799-173A-2	Sequence 2, Appli
15	81	81.8	331	2	US-09-170-042A-2	Sequence 2, Appli
16	69	69.7	330	2	US-09-732-357B-13	Sequence 13, Appl
17	50	50.5	1245	2	US-09-252-991A-30935	Sequence 30935, A
18	46	46.5	545	2	US-09-303-518D-54	Sequence 54, Appl
19	45	45.5	287	2	US-09-252-991A-29808	Sequence 29808, A
20	45	45.5	296	2	US-09-328-352-5366	Sequence 5366, Ap
21	44	44.4	559	2	US-09-252-991A-18444	Sequence 18444, A
22	43.5	43.9	237	2	US-09-902-540-15928	Sequence 15928, A
23	43.5	43.9	917	2	US-09-049-698-41	Sequence 41, Appl
24	43.5	43.9	919	2	US-09-991-181-379	Sequence 379, App
25	43.5	43.9	919	2	US-09-990-444-379	Sequence 379, App
26	43.5	43.9	919	2	US-09-997-333-379	Sequence 379, App
27	43.5	43.9	919	2	US-09-992-598-379	Sequence 379, App
28	43.5	43.9	919	2	US-09-989-735-379	Sequence 379, App
29	43.5	43.9	919	3	US-09-989-726-379	Sequence 379, App
30	43.5	43.9	919	3	US-09-997-514-379	Sequence 379, App
31	43.5	43.9	919	3	US-09-989-728-379	Sequence 379, App
32	43.5	43.9	919	3	US-09-997-349-379	Sequence 379, App
33	43.5	43.9	919	3	US-09-997-653-379	Sequence 379, App
34	43.5	43.9	919	3	US-09-989-293A-379	Sequence 379, App
35	43	43.4	125	2	US-10-094-749-2318	Sequence 2318, Ap
36	43	43.4	336	1	US-08-997-080-156	Sequence 156, App
37	43	43.4	336	1	US-08-997-362-156	Sequence 156, App
38	43	43.4	336	2	US-09-095-855-156	Sequence 156, App
39	42	42.4	137	2	US-09-252-991A-30971	Sequence 30971, A
40	42	42.4	159	2	US-09-621-976-5542	Sequence 5542, Ap
41	42	42.4	258	2	US-09-579-845-8	Sequence 8, Appli
42	42	42.4	275	2	US-09-510-322A-10	Sequence 10, Appl
43	42	42.4	276	2	US-09-514-768B-10	Sequence 10, Appl
44	41	41.4	168	2	US-09-489-039A-11028	Sequence 11028, A
45	41	41.4	197	2	US-09-252-991A-30299	Sequence 30299, A
46	41	41.4	258	2	US-09-579-845-7	Sequence 7, Appli
47	41	41.4	260	2	US-09-252-991A-21611	Sequence 21611, A
48	41	41.4	428	2	US-10-332-795-15	Sequence 15, Appl
49	41	41.4	487	2	US-09-579-845-14	Sequence 14, Appl
50	41	41.4	680	2	US-09-902-540-11278	Sequence 11278, A
51	41	41.4	4302	2	US-09-052-469-8	Sequence 8, Appli
52	41	41.4	4302	2	US-08-422-582-8	Sequence 8, Appli
53	41	41.4	4302	2	US-09-052-262-8	Sequence 8, Appli
54	41	41.4	4339	2	US-09-052-469-6	Sequence 6, Appli
55	41	41.4	4339	2	US-08-422-582-6	Sequence 6, Appli
56	41	41.4	4339	2	US-09-052-262-6	Sequence 6, Appli
57	40.5	40.9	86	2	US-09-252-991A-29178	Sequence 29178, A
58	40	40.4	155	2	US-09-902-540-15567	Sequence 15567, A
59	40	40.4	191	2	US-09-252-991A-18626	Sequence 18626, A
60	40	40.4	355	2	US-09-605-703B-860	Sequence 860, App

SCORE Search Results Details for Application 10616279 and Search Result us-10-616-279-2_copy_28_46.rapbn.

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OM protein - protein search, using sw model

Run on: May 25, 2006, 13:06:00 ; Search time 8.26087 Seconds
(without alignments)
25.616 Million cell updates/sec

Title: US-10-616-279-2_COPY_28_46
Perfect score: 99
Sequence: 1 PLGGESICSAGAPAKYSIT 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 56051 seqs, 11137335 residues

Total number of hits satisfying chosen parameters: 56051

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Published_Applications_AA_New:*
1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
8: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result %
Query

No.	Score	Match	Length	DB	ID	Description
1	43.5	43.9	917	7	US-11-302-678-32	Sequence 32, Appl
2	43.5	43.9	919	6	US-10-196-749-258	Sequence 258, App
3	43.5	43.9	919	7	US-11-101-316-70	Sequence 70, Appl
4	39.5	39.9	4074	6	US-10-501-834-2	Sequence 2, Appli
5	39	39.4	137	6	US-10-953-349-6725	Sequence 6725, Ap
6	39	39.4	183	6	US-10-953-349-6724	Sequence 6724, Ap
7	39	39.4	244	6	US-10-953-349-6723	Sequence 6723, Ap
8	39	39.4	327	6	US-10-953-349-8753	Sequence 8753, Ap
9	39	39.4	391	6	US-10-953-349-8752	Sequence 8752, Ap
10	39	39.4	476	6	US-10-953-349-8751	Sequence 8751, Ap
11	39	39.4	582	7	US-11-293-697-3683	Sequence 3683, Ap
12	39	39.4	1912	6	US-10-511-937-2561	Sequence 2561, Ap
13	38	38.4	159	6	US-10-953-349-37541	Sequence 37541, A
14	38	38.4	258	6	US-10-953-349-37540	Sequence 37540, A
15	38	38.4	278	6	US-10-953-349-37539	Sequence 37539, A
16	38	38.4	514	7	US-11-121-154-148	Sequence 148, App
17	37	37.4	177	7	US-11-293-697-4391	Sequence 4391, Ap
18	37	37.4	416	6	US-10-502-993-2	Sequence 2, Appli
19	36.5	36.9	159	7	US-11-293-697-2919	Sequence 2919, Ap
20	36	36.4	71	6	US-10-953-349-25287	Sequence 25287, A
21	36	36.4	71	6	US-10-953-349-26349	Sequence 26349, A
22	36	36.4	91	6	US-10-953-349-29384	Sequence 29384, A
23	36	36.4	161	7	US-11-293-697-3409	Sequence 3409, Ap
24	36	36.4	185	6	US-10-953-349-25898	Sequence 25898, A
25	36	36.4	201	6	US-10-953-349-17374	Sequence 17374, A
26	36	36.4	300	6	US-10-953-349-28850	Sequence 28850, A
27	36	36.4	511	6	US-10-953-349-6576	Sequence 6576, Ap
28	36	36.4	593	6	US-10-953-349-6575	Sequence 6575, Ap
29	36	36.4	632	6	US-10-953-349-9560	Sequence 9560, Ap
30	36	36.4	729	6	US-10-953-349-9559	Sequence 9559, Ap
31	36	36.4	746	6	US-10-953-349-6574	Sequence 6574, Ap
32	36	36.4	794	6	US-10-953-349-9558	Sequence 9558, Ap
33	35.5	35.9	272	7	US-11-293-697-3682	Sequence 3682, Ap
34	35.5	35.9	4059	6	US-10-501-834-6	Sequence 6, Appli
35	35	35.4	114	6	US-10-511-937-2537	Sequence 2537, Ap
36	35	35.4	143	7	US-11-293-697-2546	Sequence 2546, Ap
37	35	35.4	151	7	US-11-293-697-2514	Sequence 2514, Ap
38	35	35.4	154	6	US-10-953-349-21337	Sequence 21337, A
39	35	35.4	197	6	US-10-953-349-40189	Sequence 40189, A
40	35	35.4	208	6	US-10-953-349-2628	Sequence 2628, Ap
41	35	35.4	210	6	US-10-953-349-2627	Sequence 2627, Ap
42	35	35.4	252	6	US-10-953-349-24464	Sequence 24464, A
43	35	35.4	258	6	US-10-953-349-34274	Sequence 34274, A
44	35	35.4	284	6	US-10-953-349-21336	Sequence 21336, A
45	35	35.4	294	6	US-10-953-349-21335	Sequence 21335, A
46	35	35.4	323	7	US-11-293-697-4546	Sequence 4546, Ap
47	35	35.4	332	6	US-10-953-349-28795	Sequence 28795, A
48	35	35.4	349	6	US-10-953-349-14110	Sequence 14110, A
49	35	35.4	355	6	US-10-953-349-14109	Sequence 14109, A
50	35	35.4	362	6	US-10-953-349-14108	Sequence 14108, A
51	35	35.4	362	6	US-10-953-349-28794	Sequence 28794, A
52	35	35.4	419	6	US-10-953-349-16414	Sequence 16414, A
53	35	35.4	448	7	US-11-293-697-4755	Sequence 4755, Ap
54	35	35.4	450	6	US-10-953-349-32232	Sequence 32232, A
55	35	35.4	456	6	US-10-953-349-16413	Sequence 16413, A
56	35	35.4	1023	7	US-11-293-697-3123	Sequence 3123, Ap
57	35	35.4	2026	6	US-10-505-928-831	Sequence 831, App
58	35	35.4	4391	7	US-11-183-325-56	Sequence 56, Appl
59	34.5	34.8	112	6	US-10-953-349-19708	Sequence 19708, A

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OM protein - protein search, using sw model

Run on: May 25, 2006, 13:05:59 ; Search time 137.13 Seconds
(without alignments)
64.180 Million cell updates/sec

Title: US-10-616-279-2_COPY_28_46
Perfect score: 99
Sequence: 1 PLGGESICSAGAPAKYSIT 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Published_Applications_AA_Main:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	%	Query				
No.	Score	Match Length	DB	ID		Description

1	99	100.0	19	3	US-09-732-357A-8	Sequence 8, Appli
2	99	100.0	19	4	US-10-616-279-8	Sequence 8, Appli
3	99	100.0	19	4	US-10-624-884-8	Sequence 8, Appli
4	99	100.0	19	5	US-10-895-183-8	Sequence 8, Appli
5	99	100.0	331	3	US-09-732-357A-2	Sequence 2, Appli
6	99	100.0	331	4	US-10-616-279-2	Sequence 2, Appli
7	99	100.0	331	4	US-10-624-884-2	Sequence 2, Appli
8	99	100.0	331	5	US-10-895-183-2	Sequence 2, Appli
9	91	91.9	330	3	US-09-903-383-2	Sequence 2, Appli
10	91	91.9	331	3	US-09-978-295A-236	Sequence 236, App
11	91	91.9	331	3	US-09-938-418-8	Sequence 8, Appli
12	91	91.9	331	3	US-09-978-697-236	Sequence 236, App
13	91	91.9	331	3	US-09-978-192A-236	Sequence 236, App
14	91	91.9	331	3	US-09-999-832A-236	Sequence 236, App
15	91	91.9	331	3	US-09-978-189-236	Sequence 236, App
16	91	91.9	331	3	US-09-978-608A-236	Sequence 236, App
17	91	91.9	331	3	US-09-978-585A-236	Sequence 236, App
18	91	91.9	331	3	US-09-978-191A-236	Sequence 236, App
19	91	91.9	331	3	US-09-978-403A-236	Sequence 236, App
20	91	91.9	331	3	US-09-978-564A-236	Sequence 236, App
21	91	91.9	331	3	US-09-999-833A-236	Sequence 236, App
22	91	91.9	331	3	US-09-981-915A-236	Sequence 236, App
23	91	91.9	331	3	US-09-978-824-236	Sequence 236, App
24	91	91.9	331	3	US-09-918-585A-236	Sequence 236, App
25	91	91.9	331	3	US-09-999-834A-236	Sequence 236, App
26	91	91.9	331	3	US-09-978-423A-236	Sequence 236, App
27	91	91.9	331	3	US-09-978-193A-236	Sequence 236, App
28	91	91.9	331	3	US-09-999-830A-236	Sequence 236, App
29	91	91.9	331	3	US-09-978-757A-236	Sequence 236, App
30	91	91.9	331	3	US-09-978-187B-236	Sequence 236, App
31	91	91.9	331	3	US-09-978-643A-236	Sequence 236, App
32	91	91.9	331	3	US-09-978-375A-236	Sequence 236, App
33	91	91.9	331	3	US-09-978-298A-236	Sequence 236, App
34	91	91.9	331	3	US-09-978-188A-236	Sequence 236, App
35	91	91.9	331	3	US-09-978-681A-236	Sequence 236, App
36	91	91.9	331	3	US-09-978-194A-236	Sequence 236, App
37	91	91.9	331	3	US-09-999-829A-236	Sequence 236, App
38	91	91.9	331	3	US-09-978-299A-236	Sequence 236, App
39	91	91.9	331	3	US-09-978-544A-236	Sequence 236, App
40	91	91.9	331	3	US-09-978-665A-236	Sequence 236, App
41	91	91.9	331	3	US-09-978-802A-236	Sequence 236, App
42	91	91.9	331	3	US-09-970-944-12	Sequence 12, Appl
43	91	91.9	331	3	US-09-970-944-38	Sequence 38, Appl
44	91	91.9	331	3	US-09-970-944-40	Sequence 40, Appl
45	91	91.9	331	3	US-09-999-831A-236	Sequence 236, App
46	91	91.9	331	3	US-09-978-824-236	Sequence 236, App
47	91	91.9	331	4	US-10-017-081A-236	Sequence 236, App
48	91	91.9	331	4	US-10-167-749-236	Sequence 236, App
49	91	91.9	331	4	US-10-013-921A-236	Sequence 236, App
50	91	91.9	331	4	US-10-013-929A-236	Sequence 236, App
51	91	91.9	331	4	US-10-016-177A-236	Sequence 236, App
52	91	91.9	331	4	US-10-166-709A-236	Sequence 236, App
53	91	91.9	331	4	US-10-205-823-385	Sequence 385, App
54	91	91.9	331	4	US-10-143-031A-236	Sequence 236, App
55	91	91.9	331	4	US-10-143-030A-236	Sequence 236, App
56	91	91.9	331	4	US-10-002-967A-236	Sequence 236, App
57	91	91.9	331	4	US-10-017-083A-236	Sequence 236, App
58	91	91.9	331	4	US-10-145-128A-236	Sequence 236, App
59	91	91.9	331	4	US-10-017-191A-236	Sequence 236, App
60	91	91.9	331	4	US-10-143-028A-236	Sequence 236, App
61	91	91.9	331	4	US-10-143-029A-236	Sequence 236, App

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A;Cross-references: UNIPROT:P95087; UNIPARC:UPI0000165332; GB:Z83866; GB:AL123456; NII
membrane efflux protein - Streptomyces coelicolor C;Species: Streptomyces coelicolor C;Date: 05-
PIDN:CAB51438.1; GSPDB:GN00070; SCOEDB:SC4G6.15c A;Experimental source: strain A3(2) C;

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OM protein - protein search, using sw model

Run on: May 25, 2006, 12:36:56 ; Search time 23.9565 Seconds
(without alignments)
76.310 Million cell updates/sec

Title: US-10-616-279-2_COPY_28_46
Perfect score: 99
Sequence: 1 PLGGESICSAGAPAKYSIT 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	50	50.5	851	2	A83484	probable heme util
2	46	46.5	176	2	B81208	conserved hypothet
3	46	46.5	545	2	D81973	probable integral
4	45	45.5	273	2	B83551	hypothetical prote
5	44	44.4	3227	2	T37964	probable ubiquitin

6	43	43.4	25	2	S44201	HLA-DRB1 exon2 pro
7	43	43.4	277	2	S71222	xyloglucan endo-1,
8	42	42.4	156	2	A70412	hypothetical prote
9	42	42.4	263	1	KYRTB	chymotrypsin (EC 3
10	42	42.4	416	2	S52078	prostacyclin - rat
11	42	42.4	1465	2	S43529	165K protein, skel
12	41.5	41.9	245	2	S56827	conserved hypothet
13	41.5	41.9	459	2	T19110	hypothetical prote
14	41.5	41.9	521	2	T18942	3-oxoacid CoA-tran
15	41.5	41.9	790	2	H71509	phenylalanine-tRNA
16	41	41.4	99	2	H86480	10.9K hypothetical
17	41	41.4	134	2	B69156	hypothetical prote
18	41	41.4	413	2	G87299	poly A polymerase
19	41	41.4	455	2	AH2055	hypothetical prote
20	41	41.4	457	2	B87269	hypothetical prote
21	41	41.4	4302	2	A38971	polycystic kidney
22	40.5	40.9	493	2	C97605	probable serine pr
23	40.5	40.9	514	2	AE2827	serine proteinase
24	40	40.4	302	2	T50737	bacteriochlorophyl
25	40	40.4	387	2	F69304	3-ketoacyl-CoA thi
26	40	40.4	417	2	A54416	prostacyclin recep
27	40	40.4	460	2	T19111	hypothetical prote
28	40	40.4	475	2	S73746	MG294 homolog A05_
29	40	40.4	1290	2	T00018	period protein hom
30	40	40.4	1333	2	S65812	RNA-directed DNA p
31	39.5	39.9	236	2	F83083	hypothetical prote
32	39.5	39.9	367	2	B72644	probable transketo
33	39.5	39.9	387	2	AI3003	amidohydrolase [im
34	39.5	39.9	430	2	H98279	probable hydrolase
35	39.5	39.9	615	2	D83315	NADH2 dehydrogenas
36	39	39.4	68	2	T09545	metallothionein-li
37	39	39.4	108	1	KVMS09	Ig kappa chain V r
38	39	39.4	166	2	F82774	hypothetical prote
39	39	39.4	188	2	AC3613	probable s-adenosy
40	39	39.4	219	2	T09671	RPE15 protein - al
41	39	39.4	234	2	F46449	hypothetical prote
42	39	39.4	245	1	KYBOB	chymotrypsin (EC 3
43	39	39.4	295	2	C95354	probable epimerase
44	39	39.4	299	2	S60971	probable membrane
45	39	39.4	308	2	S44818	F44E2.8 protein -
46	39	39.4	329	2	AC3640	FMN adenylyltransf
47	39	39.4	329	2	B83162	molybdopterin bios
48	39	39.4	368	2	D72606	hypothetical prote
49	39	39.4	369	2	H70650	hypothetical prote
50	39	39.4	384	2	T35075	probable integral
51	39	39.4	402	2	T04348	endosperm specific
52	39	39.4	430	2	AB3147	conserved hypothet
53	39	39.4	430	2	H98140	hypothetical prote
54	39	39.4	447	2	T05003	hypothetical prote
55	39	39.4	461	2	A70837	probable proteinas
56	39	39.4	465	2	T19113	hypothetical prote
57	39	39.4	492	1	A27727	trypanothione-disu
58	39	39.4	522	2	T28113	hypothetical prote
59	39	39.4	585	2	B49596	genome polyprotein
60	39	39.4	677	2	E70722	hypothetical prote
61	39	39.4	1067	1	S62421	endopeptidase La h
62	39	39.4	1612	2	T30805	dutt1 protein - mo
63	39	39.4	1651	2	T14160	transmembrane rece
64	38.5	38.9	164	2	E75062	probable flagella-
65	38.5	38.9	681	2	AD3318	DNA primase (EC 2.
66	38	38.4	133	2	C31211	T-cell receptor be

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OM protein - protein search, using sw model

Run on: May 25, 2006, 12:28:34 ; Search time 194.957 Seconds
(without alignments)
90.150 Million cell updates/sec

Title: US-10-616-279-2_COPY_28_46
Perfect score: 99
Sequence: 1 PLGGESICSAGAPAKYSIT 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : UniProt_7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	91	91.9	331	1	SPON2_HUMAN	Q9bud6 homo sapien
2	81	81.8	331	2	Q4W5N4_HUMAN	Q4w5n4 homo sapien
3	75	75.8	331	2	Q5RFG6_PONPY	Q5rfg6 pongo pygma
4	69	69.7	330	1	SPON2_MOUSE	Q8bms2 mus musculu

5	69	69.7	330	1	SPON2_RAT	Q9wv75	rattus norv
6	69	69.7	330	2	Q8VD28_MOUSE	Q8vd28	mus musculu
7	51	51.5	313	2	Q6DCM4_XENLA	Q6dcm4	xenopus lae
8	51	51.5	1450	2	Q4SCT9_TETNG	Q4sct9	tetraodon n
9	50	50.5	606	2	Q2KF89_MAGGR	Q2kf89	magnaporthe
10	50	50.5	851	2	Q9I442_PSEAE	Q9i442	pseudomonas
11	49	49.5	269	2	Q66IB2_BRARE	Q66ib2	brachydanio
12	49	49.5	412	2	Q501Z8_BRARE	Q501z8	brachydanio
13	49	49.5	532	2	Q6CE62_YARLI	Q6ce62	yarrowia li
14	49	49.5	553	2	Q95PZ3_CAEEL	Q95pz3	caenorhabdi
15	48	48.5	456	2	Q44K09_CHRSL	Q44k09	chromohalob
16	48	48.5	765	2	Q7UBR0_SHIFL	Q7ubr0	shigella fl
17	48	48.5	765	2	Q83JU7_SHIFL	Q83ju7	shigella fl
18	48	48.5	928	2	Q32LP3_BOVIN	Q32lp3	bos taurus
19	48	48.5	991	2	Q94C44_CHLRE	Q94c44	chlamydomon
20	48	48.5	1021	2	Q5P6N2_AZOSE	Q5p6n2	azoarcus sp
21	48	48.5	1463	2	O55124_MOUSE	O55124	mus musculu
22	48	48.5	1463	2	Q3UQS9_MOUSE	Q3uqs9	mus musculu
23	48	48.5	2368	2	Q4S4K5_TETNG	Q4s4k5	tetraodon n
24	47	47.5	185	2	Q63TB9_BURPS	Q63tb9	burkholderi
25	47	47.5	284	2	Q37KV3_RHOPA	Q37kv3	rhodopseudo
26	47	47.5	321	2	Q2IID2_9DELT	Q2iid2	anaeromyxob
27	47	47.5	345	2	Q7VVT4_BORPE	Q7vvt4	bordetella
28	47	47.5	345	2	Q7WKN6_BORBR	Q7wkn6	bordetella
29	47	47.5	875	2	Q4HU86_GIBZE	Q4hu86	gibberella
30	47	47.5	1261	2	Q7S3G2_NEUCR	Q7s3g2	neurospora
31	47	47.5	1286	2	Q4P188_USTMA	Q4p188	ustilago ma
32	46.5	47.0	1258	2	Q4S9F0_TETNG	Q4s9f0	tetraodon n
33	46	46.5	176	2	Q5F6F3_NEIG1	Q5f6f3	neisseria g
34	46	46.5	176	2	Q7DDQ9_NEIMB	Q7ddq9	neisseria m
35	46	46.5	176	2	Q9JRC8_NEIMA	Q9jrc8	neisseria m
36	46	46.5	214	2	Q3J230_RHOS4	Q3j230	rhodobacter
37	46	46.5	514	2	Q2RQQ6_RHORU	Q2rqq6	rhodospiril
38	46	46.5	545	1	OXAA_NEIMA	Q9jw48	neisseria m
39	46	46.5	545	2	Q5F4W6_NEIG1	Q5f4w6	neisseria g
40	46	46.5	769	2	Q3E2U2_CHLAU	Q3e2u2	chloroflexu
41	46	46.5	1278	2	Q4BAZ6_BURVI	Q4baz6	burkholderi
42	45.5	46.0	340	2	Q922N8_MOUSE	Q922n8	mus musculu
43	45.5	46.0	402	2	Q3FZ78_9DELT	Q3fz78	pelobacter
44	45.5	46.0	612	2	Q7TPN9_MOUSE	Q7tpn9	m cdna sequ
45	45	45.5	144	2	Q3UGU2_MOUSE	Q3ugu2	mus musculu
46	45	45.5	250	2	Q4RVC6_TETNG	Q4rvc6	tetraodon n
47	45	45.5	258	2	Q4Q386_LEIMA	Q4q386	leishmania
48	45	45.5	273	2	Q9I5I0_PSEAE	Q9i5i0	pseudomonas
49	45	45.5	282	2	Q2WGE5_SELUN	Q2wge5	selaginella
50	45	45.5	335	2	Q2RRN6_RHORU	Q2rrn6	rhodospiril
51	45	45.5	384	1	MAPK3_BOVIN	Q3sy22	bos taurus
52	45	45.5	472	2	Q478P4_DECAR	Q478p4	dechloromon
53	45	45.5	503	2	Q2RWD0_RHORU	Q2rwd0	rhodospiril
54	45	45.5	593	2	Q4Q537_LEIMA	Q4q537	leishmania
55	45	45.5	885	2	Q4Q533_LEIMA	Q4q533	leishmania
56	45	45.5	1051	2	Q440L1_SOLUS	Q440l1	solibacter
57	45	45.5	1285	2	Q8K3T3_SPAJD	Q8k3t3	spalax juda
58	44.5	44.9	259	2	Q4HQQ6_CAMUP	Q4hqq6	campylobact
59	44.5	44.9	304	2	Q4S839_TETNG	Q4s839	tetraodon n
60	44.5	44.9	319	2	Q3B0K9_SYNS9	Q3b0k9	synechococc
61	44.5	44.9	327	2	Q2RTC5_RHORU	Q2rtc5	rhodospiril
62	44.5	44.9	573	2	Q8H7K9_ORYSA	Q8h7k9	oryza sativ
63	44	44.4	89	2	Q69SN1_ORYSA	Q69sn1	oryza sativ
64	44	44.4	209	1	RL19B_ARATH	Q9luq6	arabidopsis
65	44	44.4	265	2	O74696_PHANO	O74696	phaeosphaer

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OM protein - protein search, using sw model

Run on: May 25, 2006, 12:28:19 ; Search time 120.326 Seconds
(without alignments)
56.997 Million cell updates/sec

Title: US-10-616-279-2_COPY_77_91
Perfect score: 85
Sequence: 1 HSSDYSMWRKNQYVS 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : A_Geneseq_8:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	85	100.0	15	4	AAB82474	Aab82474 Human ext
2	85	100.0	15	9	ADW76929	Adw76929 Human RG1
3	85	100.0	290	2	AAW83329	Aaw83329 Human min
4	85	100.0	290	8	ADT50847	Adt50847 Cancer re
5	85	100.0	298	8	ADT50840	Adt50840 Cancer re
6	85	100.0	330	4	AAE12304	Aae12304 Human NPG
7	85	100.0	331	2	AAW23663	Aaw23663 Human neu
8	85	100.0	331	2	AAW70589	Aaw70589 Adhesion-
9	85	100.0	331	2	AAW83328	Aaw83328 Human min
10	85	100.0	331	2	AAy41721	Aay41721 Human PRO
11	85	100.0	331	2	AAW92460	Aaw92460 Human NAF
12	85	100.0	331	3	AAB33465	Aab33465 Human PRO
13	85	100.0	331	3	AAy79561	Aay79561 Cancer sp
14	85	100.0	331	3	AAB44277	Aab44277 Human PRO
15	85	100.0	331	3	AAy95349	Aay95349 Human PRO
16	85	100.0	331	4	AAM93266	Aam93266 Human pol
17	85	100.0	331	4	AAM93324	Aam93324 Human pol
18	85	100.0	331	4	AAM38872	Aam38872 Human pol
19	85	100.0	331	4	AAB82472	Aab82472 Human ext
20	85	100.0	331	5	ABG61806	Abg61806 Prostate
21	85	100.0	331	5	AAU79944	Aau79944 Human Spo
22	85	100.0	331	5	ABB77393	Abb77393 Human spo
23	85	100.0	331	5	AAE20463	Aae20463 Human tum
24	85	100.0	331	6	ABO25223	Abo25223 Novel hum
25	85	100.0	331	6	ABU72229	Abu72229 Novel hum
26	85	100.0	331	6	ABU84909	Abu84909 Human sec
27	85	100.0	331	6	ABU61107	Abu61107 Human PRO
28	85	100.0	331	6	ABU80376	Abu80376 Human sec
29	85	100.0	331	6	ABG75949	Abg75949 Human ant
30	85	100.0	331	6	ADA24775	Ada24775 Novel hum
31	85	100.0	331	6	ABO19678	Abo19678 Novel hum
32	85	100.0	331	6	ADA12436	Ada12436 Human sec
33	85	100.0	331	6	ABO19569	Abo19569 Novel hum
34	85	100.0	331	7	ADB73742	Adb73742 Human PRO
35	85	100.0	331	7	ADB76458	Adb76458 Human PRO
36	85	100.0	331	7	ADB75561	Adb75561 Prostate
37	85	100.0	331	7	ADC43884	Adc43884 Human sec
38	85	100.0	331	7	ADC61644	Adc61644 Human sec
39	85	100.0	331	7	ADC63608	Adc63608 Human sec
40	85	100.0	331	7	ADC66708	Adc66708 Human sec
41	85	100.0	331	7	ADC68832	Adc68832 Human sec
42	85	100.0	331	7	ADC62892	Adc62892 Human sec
43	85	100.0	331	7	ADC67957	Adc67957 Human sec
44	85	100.0	331	7	ADC41277	Adc41277 Human sec
45	85	100.0	331	7	ADC67332	Adc67332 Human sec
46	85	100.0	331	7	ADC62268	Adc62268 Human sec
47	85	100.0	331	7	ADC41901	Adc41901 Human sec
48	85	100.0	331	7	ADE49270	Ade49270 Human sec
49	85	100.0	331	7	ADE35324	Ade35324 Human sec
50	85	100.0	331	7	ADE16438	Ade16438 Human sec
51	85	100.0	331	7	ADD73053	Add73053 Human sec
52	85	100.0	331	7	ADD72411	Add72411 Human sec
53	85	100.0	331	7	ADE17062	Adel17062 Human sec
54	85	100.0	331	7	ADF47076	Adf47076 Human sec
55	85	100.0	331	7	ADG42579	Adg42579 Novel hum
56	85	100.0	331	7	ADG42585	Adg42585 Human ext
57	85	100.0	331	7	ADG42586	Adg42586 Human ext

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OM protein - protein search, using sw model

Run on: May 25, 2006, 12:44:44 ; Search time 30.9783 Seconds
(without alignments)
42.383 Million cell updates/sec

Title: US-10-616-279-2_COPY_77_91
Perfect score: 85
Sequence: 1 HSSDYSMWRKNQYVS 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Issued_Patents_AA:*
1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Match	Length	DB	ID	Description
No.		%				

1	85	100.0	15	2	US-09-732-357B-10	Sequence 10, Appl
2	85	100.0	330	2	US-09-371-696-2	Sequence 2, Appli
3	85	100.0	331	1	US-08-799-173A-2	Sequence 2, Appli
4	85	100.0	331	2	US-09-732-357B-2	Sequence 2, Appli
5	85	100.0	331	2	US-09-170-042A-2	Sequence 2, Appli
6	85	100.0	331	2	US-09-949-002-397	Sequence 397, App
7	85	100.0	331	2	US-09-999-833A-236	Sequence 236, App
8	85	100.0	331	2	US-09-807-200-2	Sequence 2, Appli
9	85	100.0	331	2	US-10-020-445A-236	Sequence 236, App
10	85	100.0	331	2	US-09-978-189-236	Sequence 236, App
11	85	100.0	331	2	US-10-017-085A-236	Sequence 236, App
12	85	100.0	331	3	US-10-145-129A-236	Sequence 236, App
13	85	100.0	331	3	US-10-013-929A-236	Sequence 236, App
14	85	100.0	331	3	US-10-013-917A-236	Sequence 236, App
15	85	100.0	422	2	US-09-949-002-504	Sequence 504, App
16	82	96.5	330	2	US-09-732-357B-13	Sequence 13, Appl
17	52	61.2	299	2	US-09-311-021-202	Sequence 202, App
18	44	51.8	677	2	US-09-270-767-58094	Sequence 58094, A
19	44	51.8	847	2	US-09-270-767-42783	Sequence 42783, A
20	42	49.4	25	2	US-09-270-767-58735	Sequence 58735, A
21	42	49.4	250	2	US-09-248-796A-15562	Sequence 15562, A
22	42	49.4	294	2	US-10-012-231A-123	Sequence 123, App
23	42	49.4	294	2	US-10-015-389A-123	Sequence 123, App
24	42	49.4	294	2	US-10-006-768A-123	Sequence 123, App
25	42	49.4	294	2	US-10-015-671A-123	Sequence 123, App
26	42	49.4	294	2	US-10-015-393A-123	Sequence 123, App
27	42	49.4	294	2	US-10-011-833A-123	Sequence 123, App
28	42	49.4	294	2	US-10-006-041A-123	Sequence 123, App
29	42	49.4	294	2	US-10-012-064A-123	Sequence 123, App
30	42	49.4	294	2	US-10-015-392A-123	Sequence 123, App
31	42	49.4	294	3	US-10-011-795B-123	Sequence 123, App
32	42	49.4	294	3	US-10-015-386A-123	Sequence 123, App
33	42	49.4	294	3	US-10-012-121A-123	Sequence 123, App
34	42	49.4	294	3	US-10-006-485A-123	Sequence 123, App
35	42	49.4	294	3	US-10-006-746A-123	Sequence 123, App
36	42	49.4	294	3	US-10-012-752A-123	Sequence 123, App
37	42	49.4	294	3	US-10-017-253A-123	Sequence 123, App
38	42	49.4	294	3	US-10-015-519A-123	Sequence 123, App
39	42	49.4	294	3	US-10-015-715A-123	Sequence 123, App
40	42	49.4	294	3	US-10-007-236A-123	Sequence 123, App
41	42	49.4	435	2	US-09-072-917A-9	Sequence 9, Appli
42	42	49.4	877	2	US-09-165-396-5	Sequence 5, Appli
43	42	49.4	3129	2	US-09-482-788-2	Sequence 2, Appli
44	41	48.2	149	2	US-09-270-767-47885	Sequence 47885, A
45	41	48.2	297	2	US-09-248-796A-25364	Sequence 25364, A
46	40	47.1	111	2	US-09-248-796A-21330	Sequence 21330, A
47	40	47.1	114	2	US-09-513-999C-5768	Sequence 5768, Ap
48	40	47.1	456	2	US-09-489-039A-8101	Sequence 8101, Ap
49	40	47.1	462	2	US-09-543-681A-5290	Sequence 5290, Ap
50	40	47.1	742	2	US-09-500-123-12	Sequence 12, Appl
51	40	47.1	811	2	US-09-500-123-9	Sequence 9, Appli
52	40	47.1	871	2	US-09-500-123-7	Sequence 7, Appli
53	40	47.1	1008	2	US-09-949-016-10423	Sequence 10423, A
54	39	45.9	152	2	US-09-270-767-37205	Sequence 37205, A
55	39	45.9	152	2	US-09-270-767-52422	Sequence 52422, A
56	39	45.9	163	2	US-09-328-352-7800	Sequence 7800, Ap
57	39	45.9	249	2	US-09-270-767-43254	Sequence 43254, A
58	39	45.9	281	2	US-09-248-796A-23359	Sequence 23359, A
59	39	45.9	635	2	US-09-248-796A-16944	Sequence 16944, A
60	39	45.9	1085	1	US-08-431-080-28	Sequence 28, Appl
61	39	45.9	1085	1	US-08-938-534-28	Sequence 28, Appl

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OM protein - protein search, using sw model

Run on: May 25, 2006, 13:05:59 ; Search time 108.261 Seconds
(without alignments)
64.180 Million cell updates/sec

Title: US-10-616-279-2_COPY_77_91
Perfect score: 85
Sequence: 1 HSSDYSMWKRKNQYVS 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Published_Applications_AA_Main:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	%	Query					
No.	Score	Match	Length	DB	ID	Description	

1	85	100.0	15	3	US-09-732-357A-10	Sequence 10, Appl
2	85	100.0	15	4	US-10-616-279-10	Sequence 10, Appl
3	85	100.0	15	4	US-10-624-884-10	Sequence 10, Appl
4	85	100.0	15	5	US-10-895-183-10	Sequence 10, Appl
5	85	100.0	290	4	US-10-629-952-4	Sequence 4, Appli
6	85	100.0	330	3	US-09-903-383-2	Sequence 2, Appli
7	85	100.0	331	3	US-09-732-357A-2	Sequence 2, Appli
8	85	100.0	331	3	US-09-978-295A-236	Sequence 236, App
9	85	100.0	331	3	US-09-938-418-8	Sequence 8, Appli
10	85	100.0	331	3	US-09-978-697-236	Sequence 236, App
11	85	100.0	331	3	US-09-978-192A-236	Sequence 236, App
12	85	100.0	331	3	US-09-999-832A-236	Sequence 236, App
13	85	100.0	331	3	US-09-978-189-236	Sequence 236, App
14	85	100.0	331	3	US-09-978-608A-236	Sequence 236, App
15	85	100.0	331	3	US-09-978-585A-236	Sequence 236, App
16	85	100.0	331	3	US-09-978-191A-236	Sequence 236, App
17	85	100.0	331	3	US-09-978-403A-236	Sequence 236, App
18	85	100.0	331	3	US-09-978-564A-236	Sequence 236, App
19	85	100.0	331	3	US-09-999-833A-236	Sequence 236, App
20	85	100.0	331	3	US-09-981-915A-236	Sequence 236, App
21	85	100.0	331	3	US-09-978-824-236	Sequence 236, App
22	85	100.0	331	3	US-09-918-585A-236	Sequence 236, App
23	85	100.0	331	3	US-09-999-834A-236	Sequence 236, App
24	85	100.0	331	3	US-09-978-423A-236	Sequence 236, App
25	85	100.0	331	3	US-09-978-193A-236	Sequence 236, App
26	85	100.0	331	3	US-09-999-830A-236	Sequence 236, App
27	85	100.0	331	3	US-09-978-757A-236	Sequence 236, App
28	85	100.0	331	3	US-09-978-187B-236	Sequence 236, App
29	85	100.0	331	3	US-09-978-643A-236	Sequence 236, App
30	85	100.0	331	3	US-09-978-375A-236	Sequence 236, App
31	85	100.0	331	3	US-09-978-298A-236	Sequence 236, App
32	85	100.0	331	3	US-09-978-188A-236	Sequence 236, App
33	85	100.0	331	3	US-09-978-681A-236	Sequence 236, App
34	85	100.0	331	3	US-09-978-194A-236	Sequence 236, App
35	85	100.0	331	3	US-09-999-829A-236	Sequence 236, App
36	85	100.0	331	3	US-09-978-299A-236	Sequence 236, App
37	85	100.0	331	3	US-09-978-544A-236	Sequence 236, App
38	85	100.0	331	3	US-09-978-665A-236	Sequence 236, App
39	85	100.0	331	3	US-09-978-802A-236	Sequence 236, App
40	85	100.0	331	3	US-09-970-944-12	Sequence 12, Appl
41	85	100.0	331	3	US-09-970-944-38	Sequence 38, Appl
42	85	100.0	331	3	US-09-970-944-39	Sequence 39, Appl
43	85	100.0	331	3	US-09-970-944-40	Sequence 40, Appl
44	85	100.0	331	3	US-09-999-831A-236	Sequence 236, App
45	85	100.0	331	3	US-09-978-824-236	Sequence 236, App
46	85	100.0	331	4	US-10-017-081A-236	Sequence 236, App
47	85	100.0	331	4	US-10-167-749-236	Sequence 236, App
48	85	100.0	331	4	US-10-013-921A-236	Sequence 236, App
49	85	100.0	331	4	US-10-013-929A-236	Sequence 236, App
50	85	100.0	331	4	US-10-016-177A-236	Sequence 236, App
51	85	100.0	331	4	US-10-166-709A-236	Sequence 236, App
52	85	100.0	331	4	US-10-205-823-385	Sequence 385, App
53	85	100.0	331	4	US-10-143-031A-236	Sequence 236, App
54	85	100.0	331	4	US-10-143-030A-236	Sequence 236, App
55	85	100.0	331	4	US-10-002-967A-236	Sequence 236, App
56	85	100.0	331	4	US-10-017-083A-236	Sequence 236, App
57	85	100.0	331	4	US-10-145-128A-236	Sequence 236, App
58	85	100.0	331	4	US-10-017-191A-236	Sequence 236, App
59	85	100.0	331	4	US-10-143-028A-236	Sequence 236, App
60	85	100.0	331	4	US-10-143-029A-236	Sequence 236, App
61	85	100.0	331	4	US-10-145-089A-236	Sequence 236, App

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GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 25, 2006, 13:06:00 ; Search time 6.52174 Seconds
(without alignments)
25.616 Million cell updates/sec

Title: US-10-616-279-2_COPY_77_91
Perfect score: 85
Sequence: 1 HSSDYSMWRKNQYVS 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 56051 seqs, 11137335 residues

Total number of hits satisfying chosen parameters: 56051

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Published_Applications_AA_New:*
1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
8: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result %
Query

No.	Score	Match	Length	DB	ID	Description
1	42	49.4	294	6	US-10-196-749-278	Sequence 278, App
2	42	49.4	295	1	US-09-949-925-128	Sequence 128, App
3	42	49.4	377	6	US-10-953-349-15715	Sequence 15715, A
4	40	47.1	963	7	US-11-223-738-5	Sequence 5, Appli
5	38	44.7	349	6	US-10-953-349-20252	Sequence 20252, A
6	38	44.7	354	6	US-10-505-928-866	Sequence 866, App
7	38	44.7	405	6	US-10-953-349-960	Sequence 960, App
8	38	44.7	415	6	US-10-953-349-959	Sequence 959, App
9	38	44.7	467	6	US-10-953-349-20251	Sequence 20251, A
10	38	44.7	490	6	US-10-953-349-20250	Sequence 20250, A
11	37	43.5	229	6	US-10-953-349-2040	Sequence 2040, Ap
12	37	43.5	338	6	US-10-953-349-2039	Sequence 2039, Ap
13	37	43.5	340	6	US-10-953-349-2038	Sequence 2038, Ap
14	37	43.5	3460	6	US-10-505-928-104	Sequence 104, App
15	36	42.4	180	6	US-10-953-349-7012	Sequence 7012, Ap
16	36	42.4	186	6	US-10-953-349-23754	Sequence 23754, A
17	36	42.4	298	6	US-10-953-349-7011	Sequence 7011, Ap
18	36	42.4	331	6	US-10-953-349-10129	Sequence 10129, A
19	36	42.4	346	7	US-11-293-697-3812	Sequence 3812, Ap
20	36	42.4	348	6	US-10-953-349-7010	Sequence 7010, Ap
21	36	42.4	587	6	US-10-511-937-2407	Sequence 2407, Ap
22	36	42.4	661	7	US-11-293-697-4325	Sequence 4325, Ap
23	36	42.4	1043	6	US-10-511-937-2452	Sequence 2452, Ap
24	35	41.2	143	6	US-10-953-349-26097	Sequence 26097, A
25	35	41.2	152	6	US-10-953-349-26096	Sequence 26096, A
26	35	41.2	156	6	US-10-953-349-24796	Sequence 24796, A
27	35	41.2	180	6	US-10-953-349-24795	Sequence 24795, A
28	35	41.2	325	7	US-11-293-697-3615	Sequence 3615, Ap
29	35	41.2	354	6	US-10-953-349-23264	Sequence 23264, A
30	35	41.2	365	6	US-10-953-349-15716	Sequence 15716, A
31	35	41.2	417	6	US-10-953-349-1118	Sequence 1118, Ap
32	35	41.2	424	6	US-10-953-349-1117	Sequence 1117, Ap
33	35	41.2	450	6	US-10-953-349-1116	Sequence 1116, Ap
34	35	41.2	485	6	US-10-953-349-11658	Sequence 11658, A
35	35	41.2	603	6	US-10-953-349-11657	Sequence 11657, A
36	35	41.2	703	6	US-10-953-349-11656	Sequence 11656, A
37	35	41.2	956	7	US-11-293-697-3037	Sequence 3037, Ap
38	34	40.0	314	6	US-10-501-834-220	Sequence 220, App
39	34	40.0	316	6	US-10-501-834-221	Sequence 221, App
40	34	40.0	359	6	US-10-953-349-27744	Sequence 27744, A
41	34	40.0	360	6	US-10-953-349-34996	Sequence 34996, A
42	34	40.0	390	6	US-10-953-349-27743	Sequence 27743, A
43	34	40.0	396	1	US-09-949-925-165	Sequence 165, App
44	34	40.0	432	6	US-10-953-349-34995	Sequence 34995, A
45	34	40.0	436	6	US-10-953-349-27742	Sequence 27742, A
46	34	40.0	439	6	US-10-953-349-34994	Sequence 34994, A
47	34	40.0	511	6	US-10-953-349-19020	Sequence 19020, A
48	34	40.0	589	6	US-10-953-349-19019	Sequence 19019, A
49	34	40.0	608	6	US-10-953-349-19018	Sequence 19018, A
50	34	40.0	695	7	US-11-293-697-4190	Sequence 4190, Ap
51	34	40.0	721	7	US-11-293-697-3470	Sequence 3470, Ap
52	33.5	39.4	416	7	US-11-264-784-359	Sequence 359, App
53	33	38.8	193	6	US-10-953-349-32280	Sequence 32280, A
54	33	38.8	200	6	US-10-953-349-32279	Sequence 32279, A
55	33	38.8	259	6	US-10-953-349-3044	Sequence 3044, Ap
56	33	38.8	297	7	US-11-293-697-4132	Sequence 4132, Ap
57	33	38.8	329	6	US-10-953-349-24690	Sequence 24690, A
58	33	38.8	332	6	US-10-953-349-24689	Sequence 24689, A
59	33	38.8	347	6	US-10-953-349-1330	Sequence 1330, Ap

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OM protein - protein search, using sw model

Run on: May 25, 2006, 12:36:56 ; Search time 18.913 Seconds
(without alignments)
76.310 Million cell updates/sec

Title: US-10-616-279-2_COPY_77_91
Perfect score: 85
Sequence: 1 HSSDYSMWRKNQYVS 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : PIR_80:*
1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	46	54.1	438	1	ALBH	alpha-amylase (EC
2	43.5	51.2	545	2	T40207	hypothetical prote
3	42	49.4	435	2	JC7137	alpha-amylase (EC
4	42	49.4	435	2	S12625	alpha-amylase (EC
5	42	49.4	729	2	C64854	ferric-coprogen re
6	42	49.4	729	2	H90813	outer membrane rec
7	42	49.4	729	2	D85673	outer membrane rec
8	42	49.4	877	2	S58824	probable membrane

9	42	49.4	1080	2	A71485	probable pbp2-tran
10	42	49.4	3587	2	I40486	surfactin syntheta
11	41	48.2	121	2	E97103	hypothetical prote
12	41	48.2	304	2	D82189	conserved hypothet
13	41	48.2	372	2	G89921	alanine dehydrogen
14	41	48.2	410	2	S77661	hypothetical prote
15	41	48.2	432	2	G90268	conserved hypothet
16	41	48.2	805	2	T34212	hypothetical prote
17	40	47.1	135	2	C21826	alpha-amylase (EC
18	40	47.1	153	2	A21826	alpha-amylase (EC
19	40	47.1	299	2	D82880	cytosine-specific
20	40	47.1	337	2	AD3614	glycosyl transfera
21	40	47.1	423	2	T09942	alpha-amylase (EC
22	40	47.1	427	1	ALBHB	alpha-amylase (EC
23	40	47.1	429	1	JE0406	alpha-amylase (EC
24	40	47.1	527	2	A82431	sensor protein Uhp
25	40	47.1	836	2	T42323	hypothetical prote
26	40	47.1	1179	2	T35093	DNA-directed DNA p
27	39	45.9	88	2	AF1023	hypothetical prote
28	39	45.9	111	2	B25159	13K sin operon hyp
29	39	45.9	279	2	D82243	transcription regu
30	39	45.9	379	2	T50967	probable pyruvate
31	39	45.9	425	2	S68305	gag polyprotein -
32	39	45.9	437	2	JC7138	alpha-amylase (EC
33	39	45.9	440	2	S14958	alpha-amylase (EC
34	39	45.9	446	2	H90063	hypothetical prote
35	39	45.9	494	2	T28660	probable adhesin P
36	39	45.9	568	2	T28876	hypothetical prote
37	39	45.9	1085	2	S55352	IFH1 protein - yea
38	39	45.9	1150	2	T15277	hypothetical prote
39	38	44.7	69	2	PC1257	alpha-amylase (EC
40	38	44.7	260	2	T22990	hypothetical prote
41	38	44.7	261	2	D86729	hypothetical prote
42	38	44.7	296	2	T12770	probable endonucle
43	38	44.7	347	2	T23944	hypothetical prote
44	38	44.7	393	2	S39383	cyclin CCL1 - yeas
45	38	44.7	415	2	B84544	probable WD-40 rep
46	38	44.7	424	2	JC7558	chromatin assembly
47	38	44.7	424	2	S17571	carboxypeptidase T
48	38	44.7	437	2	JT0946	alpha-amylase 3E -
49	38	44.7	439	2	T41966	hypothetical prote
50	38	44.7	450	2	C87463	hypothetical prote
51	38	44.7	473	2	F82561	hemolysin secretio
52	38	44.7	555	2	E87576	choline dehydrogen
53	38	44.7	742	2	H87441	hypothetical prote
54	38	44.7	768	2	S43567	R01H10.7 protein (
55	38	44.7	769	2	S35458	SNF2 protein homol
56	38	44.7	797	2	AH1302	primosomal replica
57	38	44.7	797	2	AH1674	primosomal replica
58	38	44.7	807	2	A38152	F-spondin - rat
59	38	44.7	812	2	F88577	protein R01H10.7 [
60	38	44.7	843	2	T16906	hypothetical prote
61	38	44.7	976	2	S35457	SNF2 protein homol
62	38	44.7	1403	2	S64142	hypothetical prote
63	38	44.7	2124	2	A28452	proteoglycan core
64	38	44.7	2132	1	A55182	aggreCAN precursor
65	38	44.7	2257	2	D86483	protein F5J5.19 [i
66	38	44.7	2359	2	E86483	probable acetyl-Co
67	38	44.7	2748	2	S57976	nuclear migration
68	37.5	44.1	423	2	A41204	carboxypeptidase B
69	37.5	44.1	493	2	G90604	hypothetical prote

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OM protein - protein search, using sw model

Run on: May 25, 2006, 12:28:34 ; Search time 153.913 Seconds
(without alignments)
90.150 Million cell updates/sec

Title: US-10-616-279-2_COPY_77_91
Perfect score: 85
Sequence: 1 HSSDYSMWRKNQYVS 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : UniProt_7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	85	100.0	331	1	SPON2_HUMAN	Q9bud6 homo sapien
2	85	100.0	331	2	Q4W5N4_HUMAN	Q4w5n4 homo sapien
3	85	100.0	331	2	Q5RFG6_PONPY	Q5rfg6 pongo pygma
4	82	96.5	289	2	Q6KAS6_MOUSE	Q6kas6 mus musculu

5	82	96.5	330	1	SPON2_MOUSE	Q8bms2	mus musculu
6	82	96.5	330	1	SPON2_RAT	Q9wv75	rattus norv
7	82	96.5	330	2	Q8VD28_MOUSE	Q8vd28	mus musculu
8	63	74.1	331	2	O42112_BRARE	O42112	brachydanio
9	57	67.1	355	2	Q4SQV5_TETNG	Q4sqv5	tetraodon n
10	55	64.7	313	2	Q6DCM4_XENLA	Q6dcm4	xenopus lae
11	49	57.6	138	2	Q82UD3_NITEU	Q82ud3	nitrosomona
12	49	57.6	420	2	O22019_CYAME	O22019	cyanidiosch
13	49	57.6	446	2	Q85G84_CYAME	Q85g84	cyanidiosch
14	49	57.6	919	2	Q2XVY3_PUCGR	Q2xvy3	puccinia gr
15	47	55.3	103	2	Q3YJU0_BIOGL	Q3yju0	biomphalari
16	47	55.3	390	2	Q7Y4U7_BPR69	Q7y4u7	bacterioph
17	47	55.3	924	2	Q56B07_TREHY	Q56b07	treponema h
18	46	54.1	438	1	AMY1_HORVU	P00693	hordeum vul
19	46	54.1	438	2	Q40017_HORVU	Q40017	hordeum vul
20	46	54.1	1453	2	Q755D1_ASHGO	Q755d1	ashbya goss
21	45	52.9	430	2	Q58TI0_9GOBI	Q58ti0	elacatinus
22	45	52.9	430	2	Q58TI1_9GOBI	Q58ti1	elacatinus
23	45	52.9	430	2	Q58TI2_9GOBI	Q58ti2	elacatinus
24	45	52.9	430	2	Q58TI3_9GOBI	Q58ti3	elacatinus
25	45	52.9	724	2	Q57QF1_SALCH	Q57qf1	salmonella
26	45	52.9	845	2	Q4QG81_LEIMA	Q4qg81	leishmania
27	44.5	52.4	1091	2	Q54M12_DICDI	Q54m12	dictyosteli
28	44	51.8	251	2	Q5FVN7_RAT	Q5fvn7	rattus norv
29	44	51.8	314	2	Q4NCJ0_9MICC	Q4ncj0	arthrobacte
30	44	51.8	376	2	Q57YS2_9TRYP	Q57ys2	trypanosoma
31	44	51.8	396	2	Q4CPW5_TRYCR	Q4cpw5	trypanosoma
32	44	51.8	396	2	Q57YS1_9TRYP	Q57ys1	trypanosoma
33	44	51.8	429	2	Q3R0P7_XYLFA	Q3r0p7	xylella fas
34	44	51.8	429	2	Q3RGQ3_XYLFA	Q3rgq3	xylella fas
35	44	51.8	434	2	O81699_AVEFA	O81699	avena fatua
36	44	51.8	434	2	Q87CW9_XYLFT	Q87cw9	xylella fas
37	44	51.8	437	2	O81700_AVEFA	O81700	avena fatua
38	44	51.8	839	2	Q8ML26_DROME	Q8ml26	drosophila
39	44	51.8	2889	2	Q38CF1_9TRYP	Q38cf1	trypanosoma
40	44	51.8	3099	2	Q7R5I4_GIALA	Q7r5i4	giardia lam
41	43.5	51.2	545	1	MED17_SCHPO	P87306	schizosacch
42	43.5	51.2	570	2	Q8D4R4_VIBVU	Q8d4r4	vibrio vuln
43	43.5	51.2	602	2	Q7MGB8_VIBVY	Q7mgb8	vibrio vuln
44	43	50.6	86	2	Q3J7I8_NITOC	Q3j7i8	nitrosococc
45	43	50.6	163	2	Q3SS72_NITWN	Q3ss72	nitrobacter
46	43	50.6	173	2	Q302Z8_STRSU	Q302z8	streptococc
47	43	50.6	185	2	Q3PNI1_NITHA	Q3pni1	nitrobacter
48	43	50.6	273	1	HIS6_METAC	Q8tt96	methanosarc
49	43	50.6	322	2	Q59WG7_CANAL	Q59wg7	candida alb
50	43	50.6	463	2	Q89KW8_BRAJA	Q89kw8	bradyrhizob
51	43	50.6	809	2	Q7NAF2_MYCGA	Q7naf2	mycoplasma
52	43	50.6	1383	2	Q3KF64_PSEPF	Q3kf64	pseudomonas
53	42	49.4	92	2	Q6DC15_BRARE	Q6dc15	brachydanio
54	42	49.4	105	2	Q739L5_BACC1	Q739l5	bacillus ce
55	42	49.4	206	2	Q99L35_MOUSE	Q99l35	mus musculu
56	42	49.4	230	2	Q7T5M1_GVCL	Q7t5m1	cryptophleb
57	42	49.4	239	2	Q8JRZ0_9BACU	Q8jrz0	phthorimaea
58	42	49.4	245	2	Q4HIG6_CAMCO	Q4hig6	campylobact
59	42	49.4	294	1	TSN15_HUMAN	O95858	homo sapien
60	42	49.4	331	2	Q3TA07_MOUSE	Q3ta07	mus musculu
61	42	49.4	411	2	Q5A3N9_CANAL	Q5a3n9	candida alb
62	42	49.4	411	2	Q5A3V3_CANAL	Q5a3v3	candida alb
63	42	49.4	422	2	Q6YQR6_ONYPE	Q6yqr6	onion yello
64	42	49.4	436	1	AM3D_ORYSA	P27933	oryza sativ
65	42	49.4	441	2	Q2ST11_MYCCA	Q2st11	mycoplasma

SCORE Search Results Details for Application 10616279 and Search Result us-10-616-279-2.rag.

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OM protein - protein search, using sw model

```
Run on:      May 25, 2006, 11:55:15 ; Search time 271.158 Seconds
              (without alignments)
              558.119 Million cell updates/sec
```

```
Title:          US-10-616-279-2
Perfect score:  1760
Sequence:       1 MENPSPAAALGKALCALLLA.....NGSPCPELEEEEAECVDPNCV 331
```

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

```
Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
```

```
Database :      A_Geneseq_8:*
1:  geneseqp1980s:*
2:  geneseqp1990s:*
3:  geneseqp2000s:*
4:  geneseqp2001s:*
5:  geneseqp2002s:*
6:  geneseqp2003as:*
7:  geneseqp2003bs:*
8:  geneseqp2004s:*
9:  geneseqp2005s:*
10: geneseqp2006s:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1760	100.0	331	4	AAB82472	Aab82472 Human ext
2	1760	100.0	331	9	ADW76921	Adw76921 Human RG1
3	1752	99.5	331	4	AAM93324	Aam93324 Human pol
4	1752	99.5	331	5	ABG61806	Abg61806 Prostate
5	1752	99.5	331	5	AAU79944	Aau79944 Human Spo
6	1752	99.5	331	5	ABB77393	Abb77393 Human spo
7	1752	99.5	331	7	ADB75561	Adb75561 Prostate
8	1752	99.5	331	7	ADG42585	Adg42585 Human ext
9	1752	99.5	331	7	ADN38814	Adn38814 Cancer/an
10	1752	99.5	331	7	ADN39877	Adn39877 Cancer/an
11	1752	99.5	331	8	ADJ75655	Adj75655 Marker ge
12	1752	99.5	331	8	ADL30814	Adl30814 Human pro
13	1752	99.5	331	8	ADO20071	Ado20071 Human PRO
14	1752	99.5	331	8	ADQ18813	Adq18813 Human sof
15	1752	99.5	331	8	ADT50838	Adt50838 Cancer re
16	1752	99.5	331	8	ADU06656	Adu06656 Novel bro
17	1752	99.5	422	8	ADR66362	Adr66362 Human pro
18	1752	99.5	422	8	ADR66704	Adr66704 Human pro
19	1749	99.4	331	4	AAM38872	Aam38872 Human pol
20	1749	99.4	444	4	AAM40658	Aam40658 Human pol
21	1747	99.3	331	3	AAV79561	Aay79561 Cancer sp
22	1747	99.3	349	9	AEA05999	Aea05999 His-tagge
23	1744	99.1	331	2	AAW70589	Aaw70589 Adhesion-
24	1744	99.1	331	2	AAV41721	Aay41721 Human PRO
25	1744	99.1	331	3	AAB33465	Aab33465 Human PRO
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31	1744	99.1	331	6	ABU72229	Abu72229 Novel hum
32	1744	99.1	331	6	ABU84909	Abu84909 Human sec
33	1744	99.1	331	6	ABU61107	Abu61107 Human PRO
34	1744	99.1	331	6	ABU80376	Abu80376 Human sec
35	1744	99.1	331	6	ABG75949	Abg75949 Human ant
36	1744	99.1	331	6	ADA24775	Ada24775 Novel hum
37	1744	99.1	331	6	ABO19678	Abo19678 Novel hum
38	1744	99.1	331	6	ADA12436	Ada12436 Human sec
39	1744	99.1	331	6	ABO19569	Abo19569 Novel hum
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43	1744	99.1	331	7	ADC61644	Adc61644 Human sec
44	1744	99.1	331	7	ADC63608	Adc63608 Human sec
45	1744	99.1	331	7	ADC66708	Adc66708 Human sec

ALIGNMENTS

RESULT 1

AAB82472

ID AAB82472 standard; protein; 331 AA.

XX

AC AAB82472;

XX

DT 22-AUG-2001 (first entry)

SCORE Search Results Details for Application 10616279 and Search Result us-10-616-279-2.ra1.

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OM protein - protein search, using sw model

Run on: May 25, 2006, 12:07:05 ; Search time 69.1921 Seconds
(without alignments)
418.728 Million cell updates/sec

Title: US-10-616-279-2
Perfect score: 1760
Sequence: 1 MENPSPAAALGKALCALLLA.....NGSPCPELEEEAECVPDNCV 331

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
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2	1752	99.5	331	2	US-09-949-002-397	Sequence 397, App
3	1747	99.3	331	2	US-09-807-200-2	Sequence 2, Appli
4	1744	99.1	331	2	US-09-999-833A-236	Sequence 236, App
5	1744	99.1	331	2	US-10-020-445A-236	Sequence 236, App
6	1744	99.1	331	2	US-09-978-189-236	Sequence 236, App
7	1744	99.1	331	2	US-10-017-085A-236	Sequence 236, App
8	1744	99.1	331	3	US-10-145-129A-236	Sequence 236, App
9	1744	99.1	331	3	US-10-013-929A-236	Sequence 236, App
10	1744	99.1	331	3	US-10-013-917A-236	Sequence 236, App
11	1744	99.1	422	2	US-09-949-002-504	Sequence 504, App
12	1742	99.0	331	1	US-08-799-173A-2	Sequence 2, Appli
13	1742	99.0	331	2	US-09-170-042A-2	Sequence 2, Appli
14	1551.5	88.2	330	2	US-09-371-696-2	Sequence 2, Appli
15	1506.5	85.6	330	2	US-09-732-357B-13	Sequence 13, Appl
16	1101.5	62.6	299	2	US-09-311-021-202	Sequence 202, App
17	464.5	26.4	802	1	US-07-862-021B-12	Sequence 12, Appl
18	464.5	26.4	802	1	US-08-313-288B-12	Sequence 12, Appl
19	464.5	26.4	802	5	PCT-US93-03164-12	Sequence 12, Appl
20	462.5	26.3	392	1	US-08-799-173A-7	Sequence 7, Appli
21	462.5	26.3	392	2	US-09-170-042A-7	Sequence 7, Appli
22	462.5	26.3	807	1	US-07-862-021B-10	Sequence 10, Appl
23	462.5	26.3	807	1	US-08-313-288B-10	Sequence 10, Appl
24	462.5	26.3	807	2	US-09-132-769-5	Sequence 5, Appli
25	462.5	26.3	807	5	PCT-US93-03164-10	Sequence 10, Appl
26	460.5	26.2	787	2	US-09-825-294-207	Sequence 207, App
27	460.5	26.2	787	2	US-09-970-966-207	Sequence 207, App
28	460.5	26.2	807	2	US-09-132-769-1	Sequence 1, Appli
29	460.5	26.2	807	2	US-09-132-769-3	Sequence 3, Appli
30	460.5	26.2	807	2	US-09-640-173-186	Sequence 186, App
31	460.5	26.2	807	2	US-09-713-550-186	Sequence 186, App
32	460.5	26.2	807	2	US-09-825-294-186	Sequence 186, App
33	460.5	26.2	807	2	US-09-970-966-186	Sequence 186, App
34	438.5	24.9	819	2	US-09-270-767-42963	Sequence 42963, A
35	422.5	24.0	677	2	US-09-270-767-58094	Sequence 58094, A
36	422.5	24.0	847	2	US-09-270-767-42783	Sequence 42783, A
37	420.5	23.9	132	2	US-09-022-238-2	Sequence 2, Appli
38	331	18.8	568	1	US-07-862-021B-14	Sequence 14, Appl
39	331	18.8	568	5	PCT-US93-03164-14	Sequence 14, Appl
40	309	17.6	53	1	US-08-799-173A-18	Sequence 18, Appl
41	309	17.6	53	2	US-09-170-042A-19	Sequence 19, Appl
42	189	10.7	37	2	US-09-022-238-3	Sequence 3, Appli
43	181	10.3	37	2	US-09-371-696-3	Sequence 3, Appli
44	134	7.6	1588	3	US-10-000-512-2	Sequence 2, Appli
45	130.5	7.4	56	1	US-07-862-021B-19	Sequence 19, Appl

ALIGNMENTS

RESULT 1

US-09-732-357B-2

; Sequence 2, Application US/09732357B

; Patent No. 6682902

; GENERAL INFORMATION:

; APPLICANT: Harkins, Richard

; APPLICANT: Parkes, Deborah

; APPLICANT: Parry, Gordon

; APPLICANT: Schneider, Douglas

; APPLICANT: Steinbrecher, Renate

SCORE Search Results Details for Application 10616279 and Search Result us-10-616-279-2.ra

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OM protein - protein search, using sw model

Run on: May 25, 2006, 12:23:39 ; Search time 230.952 Seconds
(without alignments)
663.879 Million cell updates/sec

Title: US-10-616-279-2
Perfect score: 1760
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	1760	100.0	331	4	US-10-624-884-2	Sequence 2, Appli

4	1760	100.0	331	5	US-10-895-183-2	Sequence 2, Appli
5	1752	99.5	331	3	US-09-970-944-12	Sequence 12, Appl
6	1752	99.5	331	3	US-09-970-944-38	Sequence 38, Appl
7	1752	99.5	331	4	US-10-205-823-385	Sequence 385, App
8	1752	99.5	331	4	US-10-295-027-132	Sequence 132, App
9	1752	99.5	331	4	US-10-295-027-1195	Sequence 1195, Ap
10	1752	99.5	331	5	US-10-723-860-1632	Sequence 1632, Ap
11	1752	99.5	331	5	US-10-631-467-907	Sequence 907, App
12	1752	99.5	331	6	US-11-051-454-385	Sequence 385, App
13	1752	99.5	331	6	US-11-203-526-40	Sequence 40, Appl
14	1747	99.3	331	5	US-10-929-973-2	Sequence 2, Appli
15	1747	99.3	349	5	US-10-919-215-1	Sequence 1, Appli
16	1744	99.1	331	3	US-09-978-295A-236	Sequence 236, App
17	1744	99.1	331	3	US-09-938-418-8	Sequence 8, Appli
18	1744	99.1	331	3	US-09-978-697-236	Sequence 236, App
19	1744	99.1	331	3	US-09-978-192A-236	Sequence 236, App
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44	1744	99.1	331	3	US-09-978-299A-236	Sequence 236, App
45	1744	99.1	331	3	US-09-978-544A-236	Sequence 236, App

ALIGNMENTS

RESULT 1

US-09-732-357A-2

; Sequence 2, Application US/09732357A

; Patent No. US20020004047A1

; GENERAL INFORMATION:

; APPLICANT: Harkins, Richard

; APPLICANT: Parkes, Deborah

; APPLICANT: Parry, Gordon

; APPLICANT: Schneider, Douglas

; APPLICANT: Steinbrecher, Renate

; TITLE OF INVENTION: DNA Encoding a No. US20020004047A1e1 RG-1 Polypeptide

; FILE REFERENCE: 51791AUSM1

; CURRENT APPLICATION NUMBER: US/09/732,357A

; CURRENT FILING DATE: 2001-05-14

SCORE Search Results Details for Application 10616279 and Search Result us-10-616-279-2.ra

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OM protein - protein search, using sw model

Run on: May 25, 2006, 12:23:59 ; Search time 14.9605 Seconds
(without alignments)
246.414 Million cell updates/sec

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Perfect score: 1760
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Gapop 10.0 , Gapext 0.5

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	98	5.6	1126	7	US-11-293-697-3665	Sequence 3665, Ap
4	83.5	4.7	548	6	US-10-548-484-78	Sequence 78, Appl
5	83	4.7	778	7	US-11-293-697-3043	Sequence 3043, Ap
6	81	4.6	406	6	US-10-953-349-31643	Sequence 31643, A
7	80.5	4.6	343	6	US-10-953-349-26233	Sequence 26233, A
8	80.5	4.6	743	7	US-11-293-697-4198	Sequence 4198, Ap
9	80	4.5	341	6	US-10-196-749-224	Sequence 224, App
10	79.5	4.5	258	6	US-10-196-749-284	Sequence 284, App
11	79.5	4.5	612	6	US-10-953-349-19032	Sequence 19032, A
12	79.5	4.5	631	6	US-10-953-349-19031	Sequence 19031, A
13	79.5	4.5	661	6	US-10-953-349-19030	Sequence 19030, A
14	79	4.5	429	6	US-10-953-349-32400	Sequence 32400, A
15	79	4.5	786	6	US-10-953-349-9018	Sequence 9018, Ap
16	78.5	4.5	694	6	US-10-505-928-312	Sequence 312, App
17	78	4.4	406	7	US-11-185-204A-2	Sequence 2, Appli
18	78	4.4	406	7	US-11-185-215A-2	Sequence 2, Appli
19	78	4.4	496	7	US-11-293-697-2541	Sequence 2541, Ap
20	78	4.4	582	7	US-11-293-697-3683	Sequence 3683, Ap
21	77.5	4.4	213	6	US-10-953-349-28731	Sequence 28731, A
22	77.5	4.4	213	6	US-10-953-349-33732	Sequence 33732, A
23	77.5	4.4	243	6	US-10-953-349-28730	Sequence 28730, A
24	77	4.4	612	6	US-10-953-349-11169	Sequence 11169, A
25	77	4.4	620	7	US-11-293-697-3458	Sequence 3458, Ap
26	77	4.4	634	6	US-10-953-349-11168	Sequence 11168, A
27	77	4.4	650	6	US-10-953-349-11167	Sequence 11167, A
28	76.5	4.3	369	7	US-11-293-697-3622	Sequence 3622, Ap
29	76.5	4.3	473	6	US-10-953-349-10337	Sequence 10337, A
30	76.5	4.3	491	6	US-10-953-349-10336	Sequence 10336, A
31	76.5	4.3	506	6	US-10-953-349-10335	Sequence 10335, A
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33	76	4.3	613	7	US-11-293-697-4125	Sequence 4125, Ap
34	76	4.3	639	7	US-11-246-999-33	Sequence 33, Appl
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37	75.5	4.3	293	6	US-10-953-349-31470	Sequence 31470, A
38	75.5	4.3	410	6	US-10-953-349-36013	Sequence 36013, A
39	75.5	4.3	448	6	US-10-953-349-36012	Sequence 36012, A
40	75	4.3	149	6	US-10-953-349-25513	Sequence 25513, A
41	75	4.3	171	6	US-10-953-349-21189	Sequence 21189, A
42	75	4.3	180	6	US-10-953-349-21188	Sequence 21188, A
43	75	4.3	187	6	US-10-953-349-21187	Sequence 21187, A
44	75	4.3	210	6	US-10-953-349-21439	Sequence 21439, A
45	75	4.3	260	6	US-10-953-349-25808	Sequence 25808, A

ALIGNMENTS

RESULT 1

US-11-293-697-4829

; Sequence 4829, Application US/11293697

; Publication No. US20060105376A1

; GENERAL INFORMATION:

; APPLICANT: HELIX RESEARCH INSTITUTE

; TITLE OF INVENTION: Novel full length cDNA

; FILE REFERENCE: H1-A0106

; CURRENT APPLICATION NUMBER: US/11/293,697

; CURRENT FILING DATE: 2005-12-05

; PRIOR APPLICATION NUMBER: US/10/108,260

; PRIOR FILING DATE: 2002-03-28

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This page gives you Search Results detail for the Application 10616279 and Search Result us-10-6:
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OM protein - protein search, using sw model

Run on: May 25, 2006, 12:00:39 ; Search time 44.8814 Seconds
(without alignments)
709.599 Million cell updates/sec

Title: US-10-616-279-2
Perfect score: 1760
Sequence: 1 MENPSPAAALGKALCALLLA.....NGSPCPELEEEAECVPDNCV 331

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: pir2:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	462.5	26.3	807	2	A38152	F-spondin - rat
2	448.5	25.5	803	2	A47723	F-spondin precurs
3	401	22.8	805	2	T34212	hypothetical prote
4	122.5	7.0	741	2	I48694	probable transcrip
5	117.5	6.7	770	2	D89447	protein F57C12.1 [
6	112	6.4	772	2	A55004	transcription fact
7	108	6.1	123	2	S49108	TRAP-C2 protein -
8	107	6.1	808	2	T10171	phospholipase D (E

9	104.5	5.9	440	2	T24232	hypothetical prote
10	103	5.9	742	2	A49672	transcription fact
11	102	5.8	1251	2	A57293	latent transformin
12	100.5	5.7	810	2	D96566	hypothetical prote
13	100.5	5.7	2957	2	T33152	hypothetical prote
14	99.5	5.7	590	2	I46687	complement compone
15	99.5	5.7	724	2	A48569	antigen Em100 - Ei
16	99.5	5.7	812	2	T03659	phospholipase D (E
17	98	5.6	903	2	T00705	N-chimerin homolog
18	97.5	5.5	808	2	T04092	phospholipase D (E
19	97	5.5	534	2	T41081	hypothetical prote
20	97	5.5	1360	2	T33922	hypothetical prote
21	96.5	5.5	598	2	A57249	beta-galactosidase
22	96.5	5.5	712	2	A45638	immunodominant mic
23	96.5	5.5	812	2	T03402	probable phospholi
24	96.5	5.5	912	2	A54423	brevican precursor
25	96.5	5.5	1572	2	T00027	brain-specific ang
26	96	5.5	591	1	C8HUB	complement C8 beta
27	96	5.5	1584	2	T00026	brain-specific ang
28	94	5.3	809	2	T11695	phospholipase D (E
29	93	5.3	483	1	VCBPI3	minor coat protein
30	92	5.2	1306	2	S25370	MSB2 protein - yea
31	91.5	5.2	424	2	C70651	hypothetical prote
32	91	5.2	152	2	D89753	protein F11C7.2 [i
33	91	5.2	862	2	T46289	hypothetical prote
34	91	5.2	937	2	D87483	ribonucleotide red
35	90	5.1	497	2	T41015	proline rich prote
36	90	5.1	692	2	AD1857	hypothetical prote
37	90	5.1	1444	2	T18856	angiogenesis inhib
38	90	5.1	1666	2	T43169	hypothetical prote
39	90	5.1	2265	1	FNBO	fibronectin - bovi
40	90	5.1	3027	2	JQ1917	polyprotein - pars
41	89.5	5.1	919	2	T32541	unc-5 protein - Ca
42	89.5	5.1	947	1	B44294	unc-5 protein, lon
43	89	5.1	649	2	D96025	probable adenylate
44	89	5.1	697	2	T03834	nuclear distributi
45	89	5.1	1257	2	T09493	period protein hom

ALIGNMENTS

RESULT 1

A38152

F-spondin - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004

C;Accession: A38152

R;Klar, A.; Baldassare, M.; Jessell, T.M.

Cell 69, 95-110, 1992

A;Title: F-spondin: a gene expressed at high levels in the floor plate encodes a secre

A;Reference number: A38152; MUID:92208952; PMID:1555244

A;Accession: A38152

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-807

A;Cross-references: UNIPROT:P35446; UNIPARC:UPI000012AC71; GB:M88469; NID:g204176; PID

A;Experimental source: embryo floor plate

A;Note: sequence extracted from NCBI backbone (NCBIN:90877, NCBIP:90878)

C;Superfamily: F-spondin; thrombospondin type 1 repeat homology

F;441-495/Domain: thrombospondin type 1 repeat homology

SCORE Search Results Details for Application 10616279 and Search Result us-10-616-279-2.rup.

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GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 25, 2006, 11:55:28 ; Search time 359.051 Seconds
(without alignments)
852.749 Million cell updates/sec

Title: US-10-616-279-2
Perfect score: 1760
Sequence: 1 MENPSPAAALGKALCALLLA.....NGSPCPELEEEAECPDNCV 331

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	1744	99.1	331	1	SPON2_HUMAN	Q9bud6 homo sapien
2	1742	99.0	331	2	Q4W5N4_HUMAN	Q4w5n4 homo sapien
3	1716	97.5	331	2	Q5RFG6_PONPY	Q5rfg6 pongo pygma
4	1506.5	85.6	330	1	SPON2_RAT	Q9wv75 rattus norv

5	1494.5	84.9	330	1	SPON2_MOUSE	Q8bms2	mus	musculu
6	1488.5	84.6	330	2	Q8VD28_MOUSE	Q8vd28	mus	musculu
7	1403	79.7	289	2	Q6KAS6_MOUSE	Q6kas6	mus	musculu
8	1113.5	63.3	313	2	Q6DCM4_XENLA	Q6dcm4	xenopus	lae
9	1108	63.0	331	2	O42112_BRARE	O42112	brachydanio	
10	1073.5	61.0	355	2	Q4SQV5_TETNG	Q4sqv5	tetraodon	n
11	871	49.5	334	2	O42111_BRARE	O42111	brachydanio	
12	733	41.6	280	2	Q4SDS0_TETNG	Q4sds0	tetraodon	n
13	568	32.3	129	2	Q3TEM5_MOUSE	Q3tem5	mus	musculu
14	522.5	29.7	601	2	Q9V746_DROME	Q9v746	drosophila	
15	512	29.1	598	2	O02029_DROME	O02029	drosophila	
16	483.5	27.5	557	2	Q4SPB7_TETNG	Q4spb7	tetraodon	n
17	470.5	26.7	808	2	O42113_BRARE	O42113	brachydanio	
18	468.5	26.6	806	2	Q4SOW9_TETNG	Q4sow9	tetraodon	n
19	466	26.5	729	2	Q69ZZ7_MOUSE	Q69zz7	mus	musculu
20	464.5	26.4	802	1	SPON1_CHICK	Q9w770	gallus	gall
21	462.5	26.3	807	1	SPON1_MOUSE	Q8vcc9	mus	musculu
22	462.5	26.3	807	1	SPON1_RAT	P35446	rattus	norv
23	462.5	26.3	807	2	Q3B7D6_RAT	Q3b7d6	rattus	norv
24	460.5	26.2	807	1	SPON1_BOVIN	Q9glx9	bos	taurus
25	460.5	26.2	807	1	SPON1_HUMAN	Q9hcb6	homo	sapien
26	457	26.0	898	2	O76822_BRAFL	O76822	branchiosto	
27	448.5	25.5	803	1	SPON1_XENLA	P35447	xenopus	lae
28	447	25.4	628	2	Q7KRF4_DROME	Q7krf4	drosophila	
29	447	25.4	763	2	Q9XZD0_DROME	Q9xzd0	drosophila	
30	443	25.2	803	2	O42114_BRARE	O42114	brachydanio	
31	441.5	25.1	873	2	Q7KR42_DROME	Q7kr42	drosophila	
32	440.5	25.0	505	2	Q5TN62_ANOGA	Q5tn62	anopheles	g
33	440.5	25.0	845	2	Q7Q082_ANOGA	Q7q082	anopheles	g
34	439.5	25.0	781	2	Q7PZ75_ANOGA	Q7pz75	anopheles	g
35	436	24.8	632	2	Q5TMM3_ANOGA	Q5tmm3	anopheles	g
36	424.5	24.1	839	2	Q8ML26_DROME	Q8ml26	drosophila	
37	420.5	23.9	216	2	Q9H7I1_HUMAN	Q9h7i1	homo	sapien
38	401	22.8	819	2	Q19305_CAEEL	Q19305	caenorhabdi	
39	400	22.7	820	2	Q61C53_CAEER	Q61c53	caenorhabdi	
40	374	21.2	924	2	Q3ZAL6_DROME	Q3zal6	drosophila	
41	306	17.4	861	2	Q8ML27_DROME	Q8ml27	drosophila	
42	280.5	15.9	549	2	Q8T988_DROME	Q8t988	drosophila	
43	271.5	15.4	461	2	Q95S22_DROME	Q95s22	drosophila	
44	225.5	12.8	92	2	Q6DC15_BRARE	Q6dc15	brachydanio	
45	167.5	9.5	78	2	Q4SDS1_TETNG	Q4sds1	tetraodon	n

ALIGNMENTS

RESULT 1

SPON2_HUMAN

ID SPON2_HUMAN STANDARD; PRT; 331 AA.

AC Q9BUD6; Q9ULW1;

DT 27-SEP-2004, integrated into UniProtKB/Swiss-Prot.

DT 01-JUN-2001, sequence version 1.

DT 07-FEB-2006, entry version 30.

DE Spondin-2 precursor (Mindin) (Differentially expressed in cancerous

DE and noncancerous lung cells 1) (DIL-1).

GN Name=SPON2; Synonyms=DIL1; ORFNames=UNQ435/PRO866;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;

OC Homo.

OX NCBI_TaxID=9606;